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QY      1224  CACCACTGTGCGGGGTGAGCTCTGAGGCTGCTGCTGCTGCTGAGGGGGGGCTGTGCG 1283
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Db      1263  TCATGCACTTCTCTCTCTCTCCACCTCTGAGAGAGAGAGGCTTGTGCTGACACCA 1322
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LOCUS   BC000407
DEFINITION Home sapiens synaptogyrin 2, mRNA (cDNA clone MGC:8571
VERSION BC000407
KEYWORDS complete cds.
SOURCE  MGC.
ORGANISM Homo sapiens (human)
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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          Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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TITLE
JOURNAL
MEDLINE
PUBMED
AUTHORS
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JOURNAL
REMARK
COMMENT
On Nov 6, 2003 this sequence version replaced gi:12653276.
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hghri.nih.gov
Ahter,N., Ayle,K., Beckstrom-Stenberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietch,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Mastello,C., Maskett,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantrilop,S., Thomas,P.J., Touchman,J.W.,
Tsurgren,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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10..684
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misc\_feature



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Dp	445	AGCTCTTGCACCTTGTGTGTGTGTGTCTTCTCTTCCACCAACAGTGGGAGT	504
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Parent No. 6342561  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08

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EARLIER APPLICATION NUMBER: 60/0522,793
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-09-12
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SEQ ID NO: 83
LENGTH: 1977
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (664)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Searched: 389414 seqs, 51625971 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	558	46.9	231	2	US-08-700-637-3
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7	93	7.8	17	4	US-09-874-923-121
8	86	7.2	17	4	US-09-227-357-511
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14	84	7.1	419	3	US-08-933-750C-30
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17	81.5	6.8	521	4	US-09-197-503-6
18	79.5	6.7	307	1	US-07-982-112-2
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21	78	6.5	871	4	US-09-500-123-7
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23	77	6.5	1214	2	US-08-231-193A-54
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#### ALIGNMENTS

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RESULT 1
US-08-700-637-2
Sequence 2, Application US/08700637
Patent No. 5854413
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Stuart, Susan G.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL SYNAPTOGRIN HOMOLOG FROM COLON
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,637
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0065 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: COLN0705
CLONE: 775426
US-08-700-637-2
Query Match 99.5%; Score 1185; DB 2; Length 224;
Best Local Similarity 99.6%; Pred. No. 3.3e-125;
Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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## RESULT 2

US-08-700-637-3  
Sequence 3, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawking, Phillip R.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Murray, Lynn E.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara U.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: GI 1072118  
US-08-700-637-3

Query March 46.9%; Score 558; DB 2; Length 231;  
Best Local Similarity 49.4%; Pred. No. 1,3e-54;  
Matches 114; Conservative 29; Mismatches 72; Indels 16; Gaps 6;  
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Db 1 MESSAGYAGAKAGSFDLRRFLTOPVAVARACVLFALIVFSICVGGYNAHESKOMYCV 60  
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Db 61 FNNRBDACRGSAIGVLAFLASAFVVDAYFPQISNATDRKXVLTGDLFLSALMTFLWF 120  
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## RESULT 3

US-09-227-357-512  
Sequence 512, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
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EARLIER APPLICATION NUMBER: 60/055,722  
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EARLIER FILING DATE: 1997-08-18  
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EARLIER APPLICATION NUMBER: 60/055,950  
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EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18

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OM protein - protein search, using sw model

Run on: April 7, 2004, 11:50:34 ; Search time 18 Seconds

(without alignments)  
647.984 Million cell updates/sec

Title: US-10-020-445a-162

Sequence: 1 MEGAYGAAKAGSFDLRRP.....QPPFQNAETGEGYQPPYV 224

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt 42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1191	100.0	224	1	SNHG2_HUMAN
2	1066	89.5	224	1	SNHG2_MOUSE
3	1055	88.6	224	1	SNHG2_RAT
4	576.5	48.4	224	1	SNHG1_HUMAN
5	576.5	48.4	224	1	SNHG1_MOUSE
6	575.5	48.3	224	1	SNHG1_RAT
7	492	41.3	229	1	SNHG1_HUMAN
8	329.5	27.7	234	1	SNHG1_HUMAN
9	257	21.6	247	1	SNHG1_MOUSE
10	150	12.6	233	1	SNHG4_MOUSE
11	103	8.6	265	1	SYNP_HUMAN
12	101	8.5	265	1	SYNP_MOUSE
13	99	8.3	265	1	SYNP_BOVIN
14	94.5	7.9	313	1	SYNP_MOUSE
15	87	7.2	208	1	CLF4_MOUSE
16	85.5	7.2	819	1	FTSK_CANCR
17	85	7.1	522	1	OCN_HUMAN
18	84.5	7.1	614	1	MAE1_HUMAN
19	83	7.0	351	1	Y876_METUA
20	83	7.0	614	1	MA3T_YEAST
21	81.5	6.8	521	1	OCN_MOUSE
22	81	6.8	718	1	TRF2_CHICK
23	80.5	6.8	602	1	MA3T_YEAST
24	80	6.7	234	1	CLF4_HUMAN
25	80	6.7	521	1	CP11_LIZSA
26	79.5	6.7	307	1	SYNP_RAT
27	79.5	6.7	507	1	Y745_CABEL
28	79	6.6	323	1	RCENM_RHOVI
29	79	6.6	451	1	CD51_RAT
30	79	6.6	469	1	NTON_BUCAT
31	79	6.6	521	1	CP11_LIZAU
32	78.5	6.6	1021	1	SL13_HUMAN
33	78.5	6.6	1419	1	ALAI_CANAL

34	77.5	6.5	282	1	UPK_MYCLE
35	77.5	6.5	452	1	YEEF_ECOLI
36	77.5	6.5	706	1	YAE4_SCHPO
37	77.5	6.5	1002	1	S123_MOUSE
38	77	6.5	281	1	UPK_CORST
39	77	6.5	367	1	CYB_AUSSTU
40	76.5	6.4	313	1	SYNP_HUMAN
41	76.5	6.4	1002	1	S123_RAT
42	76	6.4	2193	1	POLG_CX16T
43	75.5	6.3	294	1	RARD_SALTI
44	75.5	6.3	294	1	RARD_SALTY
45	75	6.3	309	1	YD22_YEAST

ALIGNMENTS

RESULT 1	SNHG2_HUMAN	STANDARD	ERT: 224 AA.
AC	043760:043762;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Synaplogyrin 2 (Cellusyrin).		
GN	SYNGR2.		
OS	Human sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98430994; PubMed=9760194;		
RA	Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,		
RA	Collins J.E., Dunham I., Blomnaw E., Roe B.A., Pfehl F.,		
RA	Dumaneski J.P.;		
RT	"Characterization of the human synaplogyrin gene family.";		
RL	Hum. Genet. 103:131-141 (1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	Tissue: lung, and lymph.		
RC	MEDLINE=22386257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditchevsky L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,		
RA	Brownstein W.J., Usdin T.B., Toshtyuk S., Carninci P., Prange C.,		
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,		
RA	Boesch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richter S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,		
RA	Schneer A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences".		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.		
CC	-1- SIMILARITY: Belongs to the synaplogyrin family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	or send an email to <a href="mailto:license@sib.ch">license@sib.ch</a> ).		

Appendix D

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CC -----
DR EMBL; AJ002308; CAA05325.1; -
DR EMBL; AJ002310; CAA05327.1; -
DR EMBL; AJ002312; CAA05327.1; JOINED.
DR EMBL; BC000407; AAH00407.1; -
DR EMBL; BC029755; AAH29755.1; -
DR Genew; HGNC:11499; SYNGR2.
DR MIM; 603926; -
DR GO; GO:0005887; C.integral to plasma membrane; TAS.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KM Transmembrane.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT CONFLICT 160 162 GVL -> VGM (IN REF. 1; CAA05327).
SQ SEQUENCE 224 AA; 24810 MW; EC92C95CEB5ED41 CRC64;

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Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKLYIGDLFSALMTFLMF 120
DB 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKLYIGDLFSALMTFLMF 120
QY 121 VGFCEFLTNQAAVTPKDVIVGADSVRAATFSFISFGVLAISAYQRYKAGVDFFION 180
DB 121 VGFCEFLTNQAAVTPKDVIVGADSVRAATFSFISFGVLAISAYQRYKAGVDFFION 180
QY 121 VGFCEFLTNQAAVTPKDVIVGADSVRAATFSFISFGVLAISAYQRYKAGVDFFION 180
DB 121 VGFCEFLTNQAAVTPKDVIVGADSVRAATFSFISFGVLAISAYQRYKAGVDFFION 180
QY 181 YVDPPTDPTNTAASYPGASVDVNYQCPPTQNAETTEGYQPPVY 224
DB 181 YVDPPTDPTNTAASYPGASVDVNYQCPPTQNAETTEGYQPPVY 224

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ID SNG2 MOUSE STANDARD; PRT; 224 AA.
AC OS510;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Synapcogyrin 2 (Cellugyrin).
GN SYNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumanski J.P.;
RT "Characterization of the human synapcogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
RN [2]
RX SEQUENCE FROM N.A.
RA Sun M.Y., Reay P.A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the synapcogyrin family.
CC -----
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DR EMBL; AJ002307; CAA05324.1; -
DR EMBL; AF151985; AAD38046.1; -
DR MGD; MGI:128324; Syng2.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KM Transmembrane.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
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SQ SEQUENCE 224 AA; 24778 MW; 951FE014C9C3EEB6 CRC64;

Query Match 89.5%; Score 1066; DB 1; Length 224;
Best Local Similarity 88.8%; Pred. No. 1.9e-89;
Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

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DB 121 VGFCEFLTNQAAVTPKDVIVGADSVRAATFSFISFGVLAISAYQRYKAGVDFFION 180
QY 181 YVDPPTDPTNTAASYPGASVDVNYQCPPTQNAETTEGYQPPVY 224
DB 181 YVDPPTDPTNTAASYPGASVDVNYQCPPTQNAETTEGYQPPVY 224

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ID SNG2 RAT STANDARD; PRT; 234 AA.
AC OS4980;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synapcogyrin 2 (Cellugyrin).
GN SYNGR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=98112834; PubMed=9446595;
RA Janz R., Stedhof T.C.;
RT "Cellugyrin, a novel ubiquitous form of synapcogyrin that is
RT phosphorylated by pp60(c-src).";
RL J. Biol. Chem. 273:2851-2857(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.
CC -1- PTM: Tyrosine phosphorylated by Src.
CC -1- SIMILARITY: Belongs to the synapcogyrin family.
CC -----
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CC -----
DR EMBL; AF039085; AAB9666.1; -
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KM Transmembrane; Phosphorylation.

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VERSION	AJ002308.1 GI:2959871		
KEYWORDS	synaptophysin 2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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TITLE	synaptophysin gene family		
REFERENCE	2 (bases 1 to 1491)		
AUTHORS	Kiedra, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-OCT-1997) Kiedra D., Dept. of Molecular Medicine, Clinical Genetics Unit, Karolinska Hospital, CMW building L-8,, S-17176 Stockholm, SWEDEN Location/Qualifiers		
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	QPPVTV		
CDS			

[illegible]

Db	783	CCAGGCCCTCTCTTTCACTGTATCCATCTGTGACAGCTACACACAGCTAAGAGCTCA	842
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Qy	924	AGCGCTCACTCTCCAGGGACCTTTTAGAAAAGGTTTTAGTAGTGTTTTCTCTGC	983
Db	903	AGCGGTCACTCTCCAGGGACCTTTTAGAAAAGGTTTTAGTAGTGTTTTCTCTGC	962
Qy	984	TTTATATGACCTCAGCCCGGCTGACAGTGGCTAAGAGCAGAGAGGGCCATGCTCT	1043
Db	963	TTTTATATGACCTCAGCCCGGCTGACAGTGGCTAAGAGCAGAGAGGGCCATGCTCT	1022
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Qy	1224	CACCAACCTGTGCGCGGTGCGCTCTGGGCTGCTCCCTGTGTGAGGGCGGGCTGTGC	1283
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Db	1443	CGGCTGGGATGCTGTTTGAGACGGATTAATGTTTCTCATCA	1488

JOURNAL	TITLE	REMARK
MEDLINE	Strausberg, R.	
PUBMED	Direct Submission	
AUTHORS	Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11X03, Bethesda, MD 20892-2590, USA	
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	On Nov 6, 2003 this sequence version replaced gi:12653276.	

REMARK	COMMENT
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> On Nov 6, 2003 this sequence version replaced gi:12653276. Contact: MGC help desk Email: <a href="mailto:gcgaps-remail.nih.gov">gcgaps-remail.nih.gov</a> Tissue Procurement: DCTD/DTP DNA Library Preparation: Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland, Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@nigri.nih.gov">nisc_mgc@nigri.nih.gov</a> Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boufiard, G.G., Breen, K., Brinkley, C.C., Brooks, S., Dietch, N.L., Granite, S., Guan, X., Gupta, J., Hachiguchi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Meduro, O.L., Masiello, C., Maskell, B., Mastrian, S.D., McCloskey, J.C., McDonnell, J., Pearson, R., Starridop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetnerby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 1 Row: k Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22091455. Location/Qualifiers 1..1708

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:8571 IMAGE:2823026"
/tissue_type="lung, small cell carcinoma"
/clone_id="NH MGC 7"
/lab_host="DH10B-R"
/note="vector: pOTB7"

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/gene="SYNR2"
/db_xref="locusid:9144"
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10..684
CDS

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/product="Gynaetogyrin 2"
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GEGSNHSESROMYCNVFNRENDCARYSAGAGVAFILASAFPLVVDAAFFPOLSNSTDKY
VLIAGDILFSLALMTFLFWGCEFLPTNOMATVNPVDVAGDSVAATLFEFSSIFSGAG
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QPPPY"
misc_feature
67..522

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/note="MARVEL": Region: Membrane-associating domain. MARVEL domain-containing proteins are often found in lipid-associating proteins - such as Occludin and MAL family proteins. It may be part of the machinery of







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2004, 11:55:09 ; Search time 23 Seconds

(without alignments)  
502.792 Million cell updates/sec

Title: US-10-020-445A-162

Perfect score: 1191

Sequence: 1 MESGAYGAKAGGSFRLRRF.....OPPTONATTEGYQPPVY 224

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1185	99.5	224	2	US-08-700-637-2
2	558	46.9	231	2	US-08-700-637-3
3	148	12.4	25	4	US-09-227-357-512
4	136	11.4	24	4	US-09-227-357-509
5	133	11.2	56	4	US-09-621-976-4130
6	93	7.8	18	4	US-09-227-357-510
7	93	7.8	18	4	US-09-874-922-121
8	86	7.2	17	4	US-09-227-357-511
9	86	7.2	17	4	US-09-328-352-6877
10	85	7.1	155	4	US-09-107-532A-5264
11	85	7.1	522	3	US-09-142-732-2
12	85	7.1	522	3	US-08-945-826-2
13	85	7.1	522	3	US-09-197-503-2
14	84	7.1	419	2	US-08-933-750C-30
15	84	7.1	419	3	US-09-234-613-30
16	81.5	6.8	521	4	US-08-945-826-6
17	81.5	6.8	521	4	US-09-197-503-6
18	79.5	6.7	307	1	US-07-982-112-2
19	79.5	6.7	576	4	US-09-540-236-2286
20	78.5	6.6	539	4	US-09-614-912-144
21	78	6.5	871	4	US-09-500-123-7
22	77	6.5	472	4	US-09-252-991A-18544
23	77	6.5	1214	2	US-08-231-193A-54
24	77	6.5	1214	2	US-08-486-273A-54
25	77	6.5	1214	3	US-08-480-474-54
26	77	6.5	1214	3	US-08-940-086A-54
27	77	6.5	1214	4	US-08-940-035A-54

28	77	6.5	1214	4	US-08-935-105A-54	Sequence 54, Appl
29	77	6.5	1214	4	US-09-648-797-54	Sequence 54, Appl
30	77	6.5	1214	4	US-09-386-123-54	Sequence 54, Appl
31	77	6.5	1231	2	US-08-231-193A-48	Sequence 48, Appl
32	77	6.5	1231	2	US-08-486-273A-48	Sequence 48, Appl
33	77	6.5	1231	3	US-08-480-474-48	Sequence 48, Appl
34	77	6.5	1231	3	US-08-940-086A-48	Sequence 48, Appl
35	77	6.5	1231	4	US-08-940-035A-48	Sequence 48, Appl
36	77	6.5	1231	4	US-08-935-105A-48	Sequence 48, Appl
37	77	6.5	1231	4	US-09-648-797-48	Sequence 48, Appl
38	77	6.5	1231	4	US-09-386-123-48	Sequence 48, Appl
39	77	6.5	1239	2	US-08-231-193A-52	Sequence 52, Appl
40	77	6.5	1239	2	US-08-486-273A-52	Sequence 52, Appl
41	77	6.5	1239	3	US-08-480-474-52	Sequence 52, Appl
42	77	6.5	1239	3	US-08-940-086A-52	Sequence 52, Appl
43	77	6.5	1239	4	US-08-940-035A-52	Sequence 52, Appl
44	77	6.5	1239	4	US-08-935-105A-52	Sequence 52, Appl
45	77	6.5	1239	4	US-09-648-797-52	Sequence 52, Appl

## ALIGNMENTS

RESULT 1  
US-08-700-637-2  
Sequence 2, Application US/08700637

Patent No. 5854413

GENERAL INFORMATION:

APPLICANT: Hawking, Phillip R.  
APPLICANT: Murray, Susan G.

APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.

STREET: 317+ Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/700,637

FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 224 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: COLNOT05

CLONE: 775426

US-08-700-637-2

Query Match 99.5%; Score 1185; DB 2; Length 224;

Best Local Similarity 99.6%; Pred. No. 3.3e-125;

Matches 223; Conservative 1; Indels 0; Gaps 0;

1 MESGAYGAKAGGSFRLRRFPOVVARVCLVFAIVFSCIVGEGYNAHESKQMYCV 60

Db 1 MESGAYGAKAGSGFDLRRLITQPQVAVARAVCLFALIVPSCITGEGYSNAHESKOMYCV 60  
QY 61 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 120  
Db 61 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 120  
QY 121 VGFCEFLNOMAVTNPKDVLVAGDSVRAAITSFISFISMGVLAAYORYKAGVDPIQN 180  
Db 121 VGFCEFLNOMAVTNPKDVLVAGDSVRAAITSFISFISMGVLAAYORYKAGVDPIQN 180  
QY 181 YVDPPTDPTNAYASYPGASVDNYQOFPPTONAEFTTEGYOPPEVY 224  
Db 181 YVDPPTDPTNAYASYPGASVDNYQOFPPTONAEFTTEGYOPPEVY 224

## RESULT 2

US-08-700-637-3  
Sequence 3, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Philip R.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL SYNAPTOGKRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Pasteo Version 1.5  
CURRENT APPLICATION DATA: 3  
APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: GI 1072118  
US-08-700-637-3

Query Match 46.9%; Score 558; DB 2; Length 211;

Best Local Similarity 49.4%; Pred. No. 1,3e-54;

Matches 114; Conservative 29; Mismatches 72; Indels 16; Gaps 6;

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Db 1 MEGGAYGAKAGSDPTLVLR---QPHILRVGWSVFSIVFGSIVNBYLNNPEEBEBCI 57  
QY 61 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 120  
Db 61 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 120  
QY 121 VGFCEFLNOMAVTNPKDVLVAGDSVRAAITSFISFISMGVLAAYORYKAGVDPIQN 180  
Db 121 VGFCEFLNOMAVTNPKDVLVAGDSVRAAITSFISFISMGVLAAYORYKAGVDPIQN 180  
QY 181 YVDPPTDPTNAYASYPGASVDNYQOFPPTONAEFTTEGYOPPEVY 224  
Db 181 YVDPPTDPTNAYASYPGASVDNYQOFPPTONAEFTTEGYOPPEVY 224

Db 118 VGFCEFLNOMAVTNPKDVLVAGDSVRAAITSFISFISMGVLAAYORYKAGVDPIQN 177  
QY 177 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 219  
Db 178 FNNEDACRYGSAIGVLAFLASAFLLVVDAYFPOISNATDRKIVIGDILFSLMTPLMF 219

## RESULT 3

US-09-227-357-512  
Sequence 512, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
EARLIER FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
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EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
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EARLIER FILING DATE: 1997-07-08  
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EARLIER FILING DATE: 1997-07-08  
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EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
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EARLIER APPLICATION NUMBER: 60/055,948  
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EARLIER APPLICATION NUMBER: 60/055,949  
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EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2004, 11:50:34 ; Search time 18 Seconds  
(without alignments)  
647.984 Million cell updates/sec

Title: US-10-020-445A-162  
Perfect score: 1191  
Sequence: 1 MSGAYGAKAGSFDLRF.....QPPTQNAETGQPPVY 224

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1191	100.0	224	1 SNG2_HUMAN	O43760 homo sapien
2	1066	89.5	224	1 SNG2_MOUSE	O54101 mus musculu
3	1055	88.6	234	1 SNG2_RAT	O54980 rattus norv
4	576.5	48.4	234	1 SNG1_HUMAN	O43759 homo sapien
5	576.5	48.4	234	1 SNG1_MOUSE	O55100 mus musculu
6	575.5	48.3	234	1 SNG1_RAT	O62876 rattus norv
7	492	41.3	229	1 SNG3_HUMAN	O43761 homo sapien
8	329.5	27.7	234	1 SNG1_MOUSE	O54101 mus musculu
9	257	21.6	247	1 SNG1_MOUSE	O76735 caenorhabdi
10	150	12.6	263	1 SNG4_MOUSE	O92112 mus musculu
11	103	8.6	255	1 SNGP_HUMAN	O68789 homo sapien
12	101	8.5	265	1 SNGP_MOUSE	P22833 rattus norv
13	99	8.3	265	1 SNGP_MOUSE	O68789 mus musculu
14	94.5	7.9	313	1 SYPH_BOVIN	P20488 bos taurus
15	87	7.3	208	1 CLF4_MOUSE	O62161 mus musculu
16	85.5	7.2	819	1 FTSK_CAUCR	O52622 caulobacter
17	85	7.1	522	1 OCLN_HUMAN	O16622 homo sapien
18	84.5	7.1	614	1 MAGT_YEAST	P15665 saccharomyc
19	83	7.0	351	1 YR76_METUA	O62829 methanococ
20	83	7.0	614	1 MAGT_YEAST	P38156 saccharomyc
21	81.5	6.8	521	1 OCLN_MOUSE	O61146 mus musculu
22	81	6.8	718	1 TRF2_CHICK	O99053 gallus gall
23	80.5	6.8	602	1 MXT_YEAST	P47186 saccharomyc
24	80	6.7	234	1 CLF4_HUMAN	O62161 mus musculu
25	80	6.7	521	1 CP11_LIZSA	O94683 liza salien
26	79.5	6.7	307	1 SYPH_RAT	P07825 rattus norv
27	79.5	6.7	507	1 YR45_CARBL	O11073 caenorhabdi
28	79	6.6	323	1 RCMV_RHOVT	P06010 rhodopsin
29	79	6.6	461	1 CDS1_RAT	O35052 r phosphati
30	79	6.6	469	1 NDNB_BUCAL	P57262 buchnera ap
31	79	6.6	521	1 CP11_LIZSA	O42231 liza aureta
32	78.5	6.6	1021	1 S123_HUMAN	P55017 homo sapien
33	78.5	6.6	1419	1 ALA1_CANAL	O13368 candida alb

34	77.5	6.5	282	1 YPR_MYCLE	P39042 mycobacteri
35	77.5	6.5	452	1 YPR_FCOIT	P33016 escherichia
36	77.5	6.5	706	1 YPR_SCHRO	O09850 schizosach
37	77.5	6.5	1002	1 S123_MOUSE	P51158 mus musculu
38	77	6.5	281	1 YPR_CORST	O94558 corynebacte
39	77	6.5	367	1 CYB_AUSST	O94113 austerlapp
40	76.5	6.4	313	1 SYPH_HUMAN	P08247 homo sapien
41	76.5	6.4	1002	1 S123_RAT	P55018 rattus norv
42	76	6.4	2193	1 POLG_COX1	O94531 c genome po
43	75.5	6.3	294	1 RAD_SALT	O82301 salmoneila
44	75.5	6.3	294	1 RAD_SALT	O94531 salmoneila
45	75	6.3	309	1 YD22_YEAST	O07651 saccharomyc

## ALIGNMENTS

RESULT 1	SNG2_HUMAN	STANDARD:	PRT:	224 AA.
AC	O43760; O43762;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Synapcogrin 2 (Cellugrylin).			
GN	SYNGR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430994; PubMed=9760194;			
RA	Kedia D., Fan H.-Q., Seroussi E., Fransson I., Guilbaud C.,			
RA	Collins J.E., Dunham I., Blenow E., Roe B.A., Piehl F.,			
RA	Dumanski J.P.;			
RT	Characterization of the human synapcogrin gene family.;			
RL	Hum. Genet. 103:131-141(1998).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Lung, and lymph;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Stapleton M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Browstein M.J., Uedlin T.B., Toshiyuki S., Carinici P., Prange C.,			
RA	Raha S.S., Louellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.V., Lu X., Gibbs R.A.,			
RA	Valley U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Butterfield A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Rodriguez J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RA	Schurich A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.			
CC	-1- SIMILARITY: Belongs to the synapcogrin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			

CC  
 DR EMBL: AJ002308; CAA05325.1; -  
 DR EMBL: AJ002310; CAA05327.1; -  
 DR EMBL: AJ002312; CAA05327.1; JOINED.  
 DR EMBL: BC000407; AAH00407.1; -  
 DR EMBL: BC029755; AAH29755.1; -  
 DR Genew: HGNC:11499; SYNGR2.  
 DR MIM: 603926; -  
 DR CO: GO:0005987; C.integral to plasma membrane; TAS.  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 KW Transmembrane.  
 FT TRANSMEM 26 46 POTENTIAL.  
 FT TRANSMEM 73 93 POTENTIAL.  
 FT TRANSMEM 105 125 POTENTIAL.  
 FT TRANSMEM 147 167 POTENTIAL.  
 FT CONFLICT 160 162 GVL->VGM (IN REF. 1: CAA05327).  
 FT SEQUENCE 224 AA; 24810 MW; EC92C95CE95BD41 CRC64;

Query Match 100.0%; Score 1191; DB 1; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-101;  
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGAGAAKAGSGFPLRRFLTPQVAVARACLVFALIVFSCITGEGYSNAHESKQMCV 60  
 DB 1 MEGAGAAKAGSGFPLRRFLTPQVAVARACLVFALIVFSCITGEGYSNAHESKQMCV 60  
 QY 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKXLYIGDLFSAWTFLMF 120  
 DB 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKXLYIGDLFSAWTFLMF 120  
 QY 121 VGCFELTNQWAVNPKDVLVGADSVRAATTFSPFISFGVLAASLAVQRYKGVDDFION 180  
 DB 121 VGCFELTNQWAVNPKDVLVGADSVRAATTFSPFISFGVLAASLAVQRYKGVDDFION 180  
 QY 181 YVPTPDPTNTAVASYPGASVDNYQCPPTQNAETTEGYPPEVY 224  
 DB 181 YVPTPDPTNTAVASYPGASVDNYQCPPTQNAETTEGYPPEVY 224

RESULT 2  
 SNG2\_MOUSE STANDARD; PRT; 224 AA.  
 ID SNG2\_MOUSE STANDARD; PRT; 224 AA.  
 AC OS5101;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Synaplogyrin 2 (Cellugyrin).  
 GN SYNGR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;

RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=98430994; Pubmed=9760194;  
 RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,  
 RA Collins J.E., Dunham I., Blennow E., Roe B.A., Pienl F.,  
 RA Dumas J.P.;  
 RT "Characterization of the human synaplogyrin gene family.";  
 RL Hum. Genet. 103:131-141 (1998).

RN [2]  
 RN SEQUENCE FROM N.A.  
 RP Sun M.Y., Reay P.A.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the synaplogyrin family.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC  
 DR EMBL: AJ002307; CAA05324.1; -  
 DR EMBL: AF151985; AAD38046.1; -  
 DR MIM: 603926; -  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 KW Transmembrane.  
 FT TRANSMEM 31 51 POTENTIAL.  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT TRANSMEM 105 125 POTENTIAL.  
 FT TRANSMEM 147 167 POTENTIAL.  
 FT SEQUENCE 224 AA; 24778 MW; 951FE014C9C3EEB6 CRC64;

Query Match 89.5%; Score 1066; DB 1; Length 224;  
 Best Local Similarity 88.8%; Pred. No. 1.9e-89;  
 Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEGAGAAKAGSGFPLRRFLTPQVAVARACLVFALIVFSCITGEGYSNAHESKQMCV 60  
 DB 1 MEGAGAAKAGSGFPLRRFLTPQVAVARACLVFALIVFSCITGEGYSNAHESKQMCV 60  
 QY 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKXLYIGDLFSAWTFLMF 120  
 DB 61 FNNEDACRYGSAIGVLAFLASAFVVDAYFPQISNATDRKXLYIGDLFSAWTFLMF 120  
 QY 121 VGCFELTNQWAVNPKDVLVGADSVRAATTFSPFISFGVLAASLAVQRYKGVDDFION 180  
 DB 121 VGCFELTNQWAVNPKDVLVGADSVRAATTFSPFISFGVLAASLAVQRYKGVDDFION 180  
 QY 181 YVPTPDPTNTAVASYPGASVDNYQCPPTQNAETTEGYPPEVY 224  
 DB 181 YVPTPDPTNTAVASYPGASVDNYQCPPTQNAETTEGYPPEVY 224

RESULT 3  
 SNG2\_RAT STANDARD; PRT; 234 AA.  
 ID SNG2\_RAT STANDARD; PRT; 234 AA.  
 AC OS4960;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Synaplogyrin 2 (Cellugyrin).  
 GN SYNGR2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;

RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Janz R., Suedhof T.C.;  
 RX MEDLINE=98112834; Pubmed=9446595;  
 RT "Cellugyrin, a novel ubiquitously form of synaplogyrin that is  
 phosphorylated by pp60(c-src)".  
 RL J. Biol. Chem. 273:2851-2857 (1998).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.  
 CC -1- PTM: Tyrosine phosphorylated by Src.  
 CC -1- SIMILARITY: Belongs to the synaplogyrin family.

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CC  
 DR EMBL: AF039085; AAB96666.1; -  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 KW Transmembrane; Phosphorylation.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2004, 11:50:34 ; Search time 18 Seconds  
(without alignments)  
647.984 Million cell updates/sec

Title: US-10-020-445a-162  
Perfect score: 1191  
Sequence: 1 MSGAGVGAAXAGGSFIDLRP.....QPPTQNAETEGYQPPVY 224

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1191	100.0	224 1	SNHG2_HUMAN
2	1066	89.5	224 1	SNHG2_MOUSE
3	1055	88.6	234 1	SNHG2_RAT
4	576.5	48.4	234 1	SNHG1_HUMAN
5	576.5	48.4	234 1	SNHG1_MOUSE
6	575.5	48.3	234 1	SNHG1_RAT
7	492	41.3	229 1	SNHG3_HUMAN
8	329.5	27.7	234 1	SNHG4_HUMAN
9	257	21.6	247 1	SNHG1_MOUSE
10	150	12.6	233 1	SNHG4_MOUSE
11	103	8.6	265 1	SYNP_HUMAN
12	101	8.5	265 1	SYNP_RAT
13	99	8.3	265 1	SYNP_MOUSE
14	94.5	7.9	313 1	SYNP_BOVIN
15	87	7.2	819 1	CLF4_MOUSE
16	85.5	7.2	208 1	FTSK_CAUCR
17	85	7.1	522 1	OC1N_HUMAN
18	84.5	7.1	614 1	MA6T_YEAST
19	83	7.0	351 1	Y876_MERIT
20	83	7.0	614 1	MA3T_YEAST
21	81.5	6.8	521 1	OC1N_MOUSE
22	81	6.8	718 1	TRF2_CHICK
23	80.5	6.8	602 1	MAXT_YEAST
24	80	6.7	234 1	CLF4_HUMAN
25	80	6.7	521 1	CP11_LIZSA
26	79.5	6.7	307 1	SYNP_RAT
27	79.5	6.7	507 1	Y745_CAREL
28	79	6.6	323 1	ROEM_RHOVI
29	79	6.6	461 1	CD31_RAT
30	79	6.6	469 1	NTON_BUCAI
31	79	6.6	521 1	CP11_LIZAU
32	78.5	6.6	1021 1	SI23_HUMAN
33	78.5	6.6	1419 1	ALAI_CANAL

34	77.5	6.5	452 1	YEFB_MYCLE
35	77.5	6.5	452 1	YEFB_ECOLI
36	77.5	6.5	706 1	YABA_SCHPO
37	77.5	6.5	1002 1	SI23_MOUSE
38	77	6.5	281 1	UPK_CORST
39	76.5	6.5	367 1	CVB_AUSHU
40	76.5	6.4	313 1	SYNP_HUMAN
41	76.5	6.4	1002 1	SI23_RAT
42	76	6.4	2193 1	POG_CX1CT
43	75.5	6.3	294 1	RARD_SALTI
44	75.5	6.3	294 1	RARD_SALTI
45	75	6.3	309 1	YD22_YEAST

## ALIGNMENTS

RESULT 1  
ID SNHG2\_HUMAN STANDARD; PRT; 224 AA.  
AC 043760; 043762;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synapcogyrin 2 (Cellulysin).  
GN SYNCR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98430994; PubMed=9760194;  
RA Keda D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,  
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,  
RA Dumanaki J.P.;  
RT "Characterization of the human synapcogyrin gene family.";  
RL Hum. Genet. 103:131-141(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, and Lymph;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Alteshtul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Koore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.T., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Wuzny D.N., Sodergren E.V., Lu X., Gibbs R.A.,  
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.  
CC -1- SIMILARITY: Belongs to the synapcogyrin family.  
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CC -----
DR EMBL; AJ002308; CAA05325.1; -
DR EMBL; AJ002310; CAA05327.1; -
DR EMBL; AJ002312; CAA05327.1; JOINED.
DR EMBL; BC000407; AAH00407.1; -
DR EMBL; BC029755; AAH29755.1; -
DR Genew; HGNC:11499; SYNGR2.
DR MIM; 603926; -
DR GO; GO:0005887; C: integral to plasma membrane; TMS.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
DR Transmembrane.
KW TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 160 162 GVL -> VGV (IN REF. 1; CAA05327).
FT CONFLICT 160 162
SQ SEQUENCE 224 AA; 24610 MW; EC92C95CE95BD41 CRC64;

Query Match
Best Local Similarity 100.0%; Score 1191; DB 1; Length 224;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAYGAAGAGGSGFDLRRLTQPOVAVARAVCLVFAIVPSCTIYGEYSNAHESKQMYCV 60
DB 1 MESSAYGAAGAGGSGFDLRRLTQPOVAVARAVCLVFAIVPSCTIYGEYSNAHESKQMYCV 60
QY 61 FNRNEDACRYGSAIGVLAFLASAFLLVVDAYFPQISNATRKYLVIQDILFSLMTFLWF 120
DB 61 FNRNEDACRYGSAIGVLAFLASAFLLVVDAYFPQISNATRKYLVIQDILFSLMTFLWF 120
QY 121 VGFCFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
DB 121 VGFCFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
QY 121 YGFFFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
DB 121 YGFFFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
QY 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
DB 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
QY 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
DB 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224

RESULT 2
SNG2 MOUSE STANDARD; PRT; 224 AA.
ID SNG2 MOUSE STANDARD; PRT; 224 AA.
AC 05101;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Synaplogyrin 2 (Cellugyrin).
GN SYNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9843094; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guillaud C.,
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dunanski J.P.;
RT "Characterization of the human synaplogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Sun M.Y., Reay P.A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the synaplogyrin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ002307; CAA05324.1; -
DR EMBL; AF151985; AAD38046.1; -
DR MGD; MGI:1328324; Syngt2.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
DR Transmembrane.
KW TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
SQ SEQUENCE 224 AA; 24778 MW; 951FE014C9C3EBE CRC64;

Query Match
Best Local Similarity 89.5%; Score 1066; DB 1; Length 224;
Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 MESSAYGAAGAGGSGFDLRRLTQPOVAVARAVCLVFAIVPSCTIYGEYSNAHESKQMYCV 60
DB 1 MESSAYGAAGAGGSGFDLRRLTQPOVAVARAVCLVFAIVPSCTIYGEYSNAHESKQMYCV 60
QY 61 FNRNEDACRYGSAIGVLAFLASAFLLVVDAYFPQISNATRKYLVIQDILFSLMTFLWF 120
DB 61 FNRNEDACRYGSAIGVLAFLASAFLLVVDAYFPQISNATRKYLVIQDILFSLMTFLWF 120
QY 121 VGFCFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
DB 121 VGFCFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
QY 121 YGFFFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
DB 121 YGFFFLTNQMAVTPKQVILVAGADSVRAAIFPSFISMGVLAASLAVQRYKAGVDPIQN 180
QY 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
DB 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
QY 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224
DB 181 YVDETPDPTNTAYASYPGASVDNYQOFPPTONAEETEGYQPPVY 224

RESULT 3
SNG2 RAT STANDARD; PRT; 224 AA.
ID SNG2 RAT STANDARD; PRT; 224 AA.
AC 054980;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synaplogyrin 2 (Cellugyrin).
GN SYNGR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112834; PubMed=9446595;
RA Tarr R., Suedhof T.C.;
RT "Cellugyrin, a novel ubiquitous form of synaplogyrin that is
RT phosphorylated by pp60(c-src).";
RL J. Biol. Chem. 273:2851-2857(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Ubiquitous; low expression in brain.
CC -1- PTM: Tyrosine phosphorylated by Src.
CC -1- SIMILARITY: Belongs to the synaplogyrin family.
CC -----
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CC -----
DR EMBL; AF039085; AAB96666.1; -
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Transmembrane; Phosphorylation.

```

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FT TRANSMEM 40 60 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
SQ SEQUENCE 234 AA; 25709 MW; 68168A787CCF5B8C CRC64;

Query Match 88.64; Score 1055; DB 1; Length 234;
Best Local Similarity 87.94; Pred. No. 2e-68;
Matches 197; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSGAGCAAGAGGSPDIREFLTOPQVAVACVFLVIFSCITYGEGYNAHESKQMYCV 60
DB 11 MSGAGCAAGAGGSPDIREFLTOPQVAVACVFLVIFSCITYGEGYNAHESKQMYCV 70
QY 61 FNNEDACRGASAGVAFAPLAFVAVDAPFOINATDRKYLIGDILFSLMTETWF 120
DB 71 FNNEDACRGASAGVAFAPLAFVAVDAPFOINATDRKYLIGDILFSLMTETWF 130
QY 121 VGFCFLTNQWAVTNPKDVLVGADSVRAATFSEFISFSGVLASLAVQRYKAGVDDEFION 180
DB 131 VGFCFLTNQWAVTNPKDVLVGADSVRAATFSEFISFSGVLASLAVQRYKAGVDDEFION 190
QY 181 YVDPDPDPTAAASYPRASVDNYQOPEFTQNAETTEGYQPPVY 224
DB 191 YVDPDPDPTAAASYPRASVDNYQOPEFTQNAETTEGYQPPVY 234

RESULT 4
SNG1_HUMAN STANDARD; PRT: 234 AA.
AC 043759; 043757; 043758; 096356; 090GZ4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptogyrin 1.
GN SYNGR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.E., Dunham I., Blomov E., Roe B.A., Pleni F.,
RA Dumanaki J.P.;
RT "Characterization of the human synaptogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smith L.J., Altschough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole G.G., Collier R.B., Connor R.,
RA Conroy D., Corry N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graihm D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hall S.E., Jones M.C., Kershaw J., Kimberley A.M., King S.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Mair J.D., Mashregh-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., Mcmurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillips R.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Scottlund C., Spigson L., Stewart C.A., Sultson J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilting L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,

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RA Miroshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Matsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenson S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Zhang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray U., Miller N., Mink P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.O., Shibuya H., Simon M.I., Dumanaki U.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:488-495(1999).
RN 13
RP SEQUENCE FROM N.A. (ISOFORM 1B).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diachenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pirange C.,
RA Rahn S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1A;
CC IsoId=043759-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=043759-2; Sequence=VSP_006332;
CC Name=1C;
CC IsoId=043759-3; Sequence=VSP_006331, VSP_006332;
CC 1- SIMILARITY: Belongs to the synaptogyrin family.
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CC or send an email to license@ebi.ac.uk).
CC EMBL; AJ002305; CA005322.1;
CC EMBL; AJ002304; CA005321.1;
CC EMBL; AJ002303; CA005320.1;
CC EMBL; AL002326; CA18451.1;
CC EMBL; AL002326; CA18451.1;
CC EMBL; AL002326; CA18451.1;
CC EMBL; AL002326; CA18451.1;
CC EMBL; BC000731; AA000731.1;
CC EMBL; HGNC:11498; SYNGR1.
CC MIM: 603925; --

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DR GC: 0005887; C: integral to plasma membrane; TMS.  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 KM Transmembrane; Synapse; Alternative splicing.  
 FT TRANSMEM 24 44 POTENTIAL.  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT TRANSMEM 104 124 POTENTIAL.  
 FT TRANSMEM 149 169 POTENTIAL.  
 FT VARSPLIC 1 33 MEGAGYAGKAGAGADPPTLVRQPHITLAVSW -> MTLT  
 EFGLEFDPMSIGSWTQFWSVSRPGE (in isoform 1C).  
 FT VARSPLIC 162 234 AGAVALAFORVQIGADSALEFSDYMDPDSMSVPAFYEP  
 NMGDPAGMGTYGCGAPNTPTDTPGQYOSGY -> SLTAA  
 LAVRFKDLSPQEBXSTLFPASAP (in isoform 1B  
 and isoform 1C).  
 FT CONFLICT 203 203 /FtId=VSP\_006332.  
 FT SEQUENCE 234 AA; 25570 MW; 8B015CEBBD461E12 CRC64; MISSING (IN REF. 2).

Query Match 48.4%; Score 576.5; DB 1; Length 234;  
 Best Local Similarity 48.8%; Pred. No. 4.1e-45;  
 Matches 113; Conservative 32; Mismatches 73; Indels 13; Gaps 4;

QY 1 MEGAGYAGKAGAGADPPTLVRQPHITLAVSW 60  
 1 MEGAGYAGKAGAGADPPTLVRQPHITLAVSWLFSTIVGSIYNEGYLNSAGESEFCI 60  
 11  
 QY 61 FNRNEDACRYGSAIGVLAFLASAFVLDVAFYPOISNATDRKYLVIQDLTSLMTFLMF 120  
 61 YNRNPNACSYGVAVGVLAFLTCLLYALDVYFPQISSVKRKAVALSDIGVSAFMAFLMF 120  
 61  
 QY 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 176  
 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 176  
 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 180  
 121  
 QY 177 FIONVVDPTDPNTAYASY-----PGASVDNYQCPPTQNAETTEGYQ 219  
 177 FIONVVDPTDPNTAYASY-----PGASVDNYQCPPTQNAETTEGYQ 219  
 181 FSDYMDPDSQSSMVPAYVPEPTGPDPAAGMGTYGQHPANTFTE-PQGYQ 230  
 181

RESULT 5  
 SINGL\_MOUSE STANDARD; PRT; 234 AA.  
 ID SINGL\_MOUSE STANDARD; PRT; 234 AA.  
 AC 055100; Q9DC90;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Synaplogyrin 1.  
 GN SYNGR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1B).  
 RA MEDLINE=98430994; PubMed=9760194;  
 RA Kedar D., Pan H.-Q., Seroussi E., Franssen I., Guilbaud C.,  
 RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,  
 RA Dumaneki J.P.;  
 RA "Characterization of the human synaplogyrin gene family";  
 RA Hum. Genet. 103:131-141(1998).  
 RL [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A AND 1B).  
 RC STRAIN=C57BL/6J; Tissue=Brain;  
 EX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai U., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 RA Flitschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,

RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Maehio T.,  
 RA Sakai K., Okido T., Furuno M., Kono H., Batdarelli R., Barch G.,  
 RA Blake U., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontecki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection";  
 RT Nature 409:685-690(2001).  
 RL Nature 409:685-690(2001).  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1A;  
 CC IsoId=O55100-1; Sequence=Displayed;  
 CC Name=1B;  
 CC IsoId=O55100-2; Sequence=VSP\_006333;  
 CC - SIMILARITY: Belongs to the synaplogyrin family.  
 CC -----  
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DR EMBL, AJ002306; CAA05323.1;  
 DR EMBL, AK002972; BAB22487.1;  
 DR EMBL, AK010442; BAB26943.1;  
 DR MGI, MGI:1328323; Syngr1.  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 KM Transmembrane; Synapse; Alternative splicing.  
 FT TRANSMEM 24 44 POTENTIAL.  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT TRANSMEM 104 124 POTENTIAL.  
 FT TRANSMEM 149 169 POTENTIAL.  
 FT VARSPLIC 162 234 AGAVALAFORVQIGADSALEFSDYMDPDSMSVPAFYEP  
 NMGDPAGMGTYGCGAPNTPTDTPGQYOSGY -> SLTAA  
 LAVRFKDLSPQEBXSTLFPASAP (in isoform 1B)  
 FT CONFLICT 203 203 /FtId=VSP\_006333.  
 FT SEQUENCE 234 AA; 25653 MW; 0956602IDF35809A CRC64; MISSING (IN REF. 2).

Query Match 48.4%; Score 576.5; DB 1; Length 234;  
 Best Local Similarity 49.8%; Pred. No. 4.1e-45;  
 Matches 115; Conservative 30; Mismatches 73; Indels 13; Gaps 5;

QY 1 MEGAGYAGKAGAGADPPTLVRQPHITLAVSW 60  
 1 MEGAGYAGKAGAGADPPTLVRQPHITLAVSWLFSTIVGSIYNEGYLNSAGESEFCI 60  
 11  
 QY 61 FNRNEDACRYGSAIGVLAFLASAFVLDVAFYPOISNATDRKYLVIQDLTSLMTFLMF 120  
 61 YNRNPNACSYGVAVGVLAFLTCLLYALDVYFPQISSVKRKAVALSDIGVSAFMAFLMF 120  
 61  
 QY 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 176  
 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 176  
 121 VGFCFLTNQMAVNTPKD--VLVGADSVRAAITSFSEFSGVLAFLAYORYAGYVD-- 180  
 121  
 QY 177 FIONVVDPTDPNTAYASY-----PGASVDNYQCPPTQNAETTEGYQ 219  
 177 FIONVVDPTDPNTAYASY-----PGASVDNYQCPPTQNAETTEGYQ 219  
 181 FSDYMDPDSQSSMVPAYVPEPTGPDPAAGMGTYGQHPANTFTE-PQGYQ 230  
 181

RESULT 6  
 SINGL\_RAT STANDARD; PRT; 234 AA.  
 ID SINGL\_RAT STANDARD; PRT; 234 AA.  
 AC 062876;



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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Synaplogyrin 1 (p29).
GN SYNGR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=96134029; PubMed=8557746;
RA Stenius K., Jahn R., Suedhof T.C., Jahn R.;
RT "Structure of synaplogyrin (p29) defines novel synaptic vesicle
   protein."
RL J. Cell Biol. 131:1801-1809(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Nervous system.
CC -1- SIMILARITY: Belongs to the synaplogyrin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U9549; AAB17890.1; -
DR InterPro: IPR008253; MARVEL; 1.
DR Pfam: PF01284; MARVEL; 1.
KW Transmembrane; Synapse.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
SQ SEQUENCE 234 AA; 25669 MW; B3038B64C49F31E1 CRC64;

Query Match 48.3%; Score 575.5; DB 1; Length 234;
Best Local Similarity 49.8%; Pred. No. 5, 1e-45;
Matches 115; Conservative 30; Mismatches 73; Indels 13; Gaps 5;

QY 1 MEGSAAGAAKAGGAFDLRFLTPQVAVARAVCLVFALIVSCYIGRYSNAHESKQMYCV 60
DB 1 MEGSAAGAGAGAGAFDPTLVVQPTTLRVSWVFSIVFGSTVMEGYLNPEESEEFCI 60
QY 61 FNRNEDACRYGSAIGVLAFLASAFPLVVDVAFPOISNATDRKYLVIIGDLLFSALMTFLWF 120
DB 61 YNRNPACSYGVTVGLAFVLCVLAIDVYFPQISSVKRKAVALSDIGVSAFNAFWF 120
QY 121 VGCFCFLTNQAVNPNPD--VLVADSVRAITSFSTISMGVLAISLAVQRYKAGYVD-- 176
DB 121 VGCFCFLTNQAVNPNPD--VLVADSVRAITSFSTISMGVLAISLAVQRYKAGYVD-- 176
QY 121 VGCFCFLTNQAVNPNPD--VLVADSVRAITSFSTISMGVLAISLAVQRYKAGYVD-- 176
DB 121 VGCFCFLTNQAVNPNPD--VLVADSVRAITSFSTISMGVLAISLAVQRYKAGYVD-- 176
QY 177 FIONVVDPTDPENTAYASY--PGASVD-----NYOQPFPTQVARTTESGYQ 219
DB 177 FIONVVDPTDPENTAYASY--PGASVD-----NYOQPFPTQVARTTESGYQ 219
DB 181 FSGQDYMDFSDSSMPAFAPYVPSAGSDPTMGSTYGHANAFDAE-PQGYQ 230

RESULT 7
SNG3_HUMAN STANDARD; PRT; 229 AA.
AC Q43761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaplogyrin 3.
GN SYNGR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=96430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumaniski J.P.;
RT "Characterization of the human synaplogyrin gene family."
RL Hum. Genet. 103:131-141(1998).
RN [2]
RP REVISIONS.
RA Kedra D.;
RL submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.R.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Huik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
   human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain and placenta.
CC -1- SIMILARITY: Belongs to the synaplogyrin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ002309; CAA05326.2; -
DR EMBL: BC014087; AAB14087.1; -
DR Genew: HGNC:11501; SYNGR3.
DR MIM: 603927; -
DR GO: G0:0005887; C: integral to plasma membrane; TMS.
DR InterPro: IPR008253; MARVEL; 1.
DR Pfam: PF01284; MARVEL; 1.
KW Transmembrane.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 70 90 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
SQ SEQUENCE 229 AA; 24555 MW; 0755812EDD4AD4C5 CRC64;

Query Match 41.3%; Score 492; DB 1; Length 229;
Best Local Similarity 45.8%; Pred. No. 1, 8e-37;
Matches 104; Conservative 30; Mismatches 87; Indels 6; Gaps 3;

QY 1 MEGSAAGAAKAGGAFDLRFLTPQVAVARAVCLVFALIVSCYIGRYSNAHESKQMYCV 60
DB 1 MEGSAAGAGAGALDVVSFAFRPQTLRLVASWVFSIAVGPVINEGYVATDSPEELRCV 60
QY 61 FNRNEDACRYGSAIGVLAFLASAFPLVVDVAFPOISNATDRKYLVIIGDLLFSALMTFLWF 120
DB 61 FNRNAGACRFVNLGLAFVLAFAFLVDVRFQGISVVRBRRAVLLDLGSGMSTFLWF 120

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QY 121 VGFPGFLINQAVNPKVVLVGA-DSVRAATFSFSSIFSGVSLAYQRYKAGVDDPQ 179
DB 121 VGFPGFLINQAVNPKVVLVGA-DSVRAATFSFSSIFSGVSLAYQRYKAGVDDPQ 180
QY 180 NYVDPPTDPTAVASYPGAS-----VDNYQOPFTQNAET-EGYQPP 221
DB 181 ATGELSTGASQAVPGYVSGVSESTETYSPPFTETLDTSPKQYQP 227

RESULT 8
SNG4 HUMAN STANDARD; PRT; 234 AA.
ID SNG4 HUMAN STANDARD; PRT; 234 AA.
AC 095473;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DB Synapcogyrin 4.
GN SNGR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kedia D., Dumanaki J.P.;
RT "Cloning of a novel member of synapcogyrin gene family.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the synapcogyrin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011733; CA009754.1; -
DR Genem; HGNC:11502; SNGR4.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Transmembrane.
FT TRANSMEM 25 45 POTENTIAL.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 145 165 POTENTIAL.
SQ SEQUENCE 234 AA; 25786 MW; 801134E4D840288F CRC64;

Query Match 27.7%; Score 329.5; DB 1; Length 234;
Best Local Similarity 35.5%; Pred. No. 9.5e-23;
Matches 70; Conservative 34; Mismatches 72; Indels 21; Gaps 2;

QY 19 FLTPQPOVAVAVCLVPAIVFSCIYGEYSNAHESKQMYCVFNRENACRYSAIGVLA 78
DB 17 QFLRPKPITTEVFEGVSLIVISLITDGYQNKESPOLCHILNSNSVACSPAVGAGFLA 76
QY 79 FLASAFILVVDVAVYPOISNATDRKYLIVIGDLFSALMTFLMPFGFGLTNQMAVTNPKQV 138
DB 77 FLSCIAFLVLDTOSTRINAGTRFKTAFOLDLITLVAWVWFGFCFLANQWQHSPPKEF 136
QY 139 LVGADSVRAATFSFSSIFSGVSLAYQRYKAGVDDPQ 183
DB 137 ILGSSAQALAFEFSSILVWIFQAVLAFQDLRNDAPVYKRFLEGGWLTTLPLPSAN 196
QY 184 -----PTDENT-AYAS 194
DB 197 SPVNMPTTGPNSLSYAS 213

RESULT 9
SNG1 CAEBL STANDARD; PRT; 247 AA.

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AC 076735; Q22340;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DB Synapcogyrin homolog.
GN SNG-1 OR T08A9.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodetinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Nonet M.;
RT "Visualization of presynaptic terminal specializations in live C.
RT elegans with synaptic vesicle protein-GFP fusions.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RA Pauley A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the synapcogyrin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF079373; AAC27798.1; -
DR EMBL; U40417; AAA81418.2; -
DR PIR; T43324; T43324.
DR WormPep; T08A9.3; CE04918.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Transmembrane.
FT TRANSMEM 25 45 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
SQ SEQUENCE 247 AA; 26792 MW; F199D0E8DEFF1E8A0 CRC64;

Query Match 21.6%; Score 257; DB 1; Length 247;
Best Local Similarity 27.2%; Pred. No. 3.7e-16;
Matches 67; Conservative 46; Mismatches 95; Indels 38; Gaps 6;

QY 5 AYGAAGAGSPDLRFLTPQVAVAVCLVPAIVFSCIYGEYSNAHESKQMYCVFNREN 64
DB 6 AYGAAGAGSPDLRFLTPQVAVAVCLVPAIVFSCIYGEYSNAHESKQMYCVFNREN 65
QY 65 EDACRYGSAIGVLAFLASAFILVVDVAVYPOISNATDRKYLIVIGDLFSALMTFLMPFGFC 124
DB 66 SSTCSFATAVGFFAVGCAIVLIVDAKMDQISSVTRRAVLADLVSAIFTAFLIGPF 125
QY 125 FLTNG---WAYTNPDVAVGADSVRAATFSFSSIFSGVSLAYQRYKAG----- 173
DB 126 TWFSKLSAEVDEDDENPTKTNNKFGILSLSLFLAGGAAPFRWKRYEIGNQATHEPN 185
QY 174 -----VDPEIQYVDPPT-----PDENTAYASYPGASVNDYQPP-----PTQNA 212
DB 186 YDEHFGQYSTDVQDGYGVDSTGIGHGADPPQSSYSS--GAAPQWTQCPSPNRYTO-- 241
QY 213 ETTGQY 218
DB 242 --SEGI 245

RESULT 10
SNG4 MOUSE

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ID  SNG4 MOUSE STANDARD; PRT; 233 AA.
AC  Q9Z1I2;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  SYNCR4.
GN  SYNCR4.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kedra D., Dumaneki J.P.;
RT  "Cloning of a novel member of synaptophysin gene family.";
RL  Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: Belongs to the synaptophysin family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: A011734; CA09755.1; -
DR  MCD; MGI:1928903; Synr4.
DR  InterPro: IPR008253; Marvel.
DR  Pfam: PF01284; MARVEL; 1.
KW  Transmembrane.
SQ  SEQUENCE 233 AA; 25650 MW; 2A60443CB50ED77 CRC64;

Query Match 12.6%; Score 150; DB 1; Length 233;
Best Local Similarity 39.7%; Pred. No. 1.7e-06;
Matches 29; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 19 REFLOPQVAVAVCLVFLVPSGIVGEGSYNAHESKQVYCVFNREDACRYGSAIGVLA 78
DB 17 RFRARRKSRISIRFGVLSLVTLISLTDGQNRTEPQRCVLNSHMAQCSFVAVGAGFLS 76
QY 79 FLASAFFLVVDAY 91
DB 77 FLSCVFLVLAIDAY 89

RESULT 11
SYNP_HUMAN STANDARD; PRT; 265 AA.
AC  Q8TBG9;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  SYNAPTOPORIN.
GN  SYNPR.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Mao Y., Xie Y., Cheng C.;
RT  "Cloning and characterization of a novel human synaptophysin-like
RT  protein." (OCT-2002) to the EMBL/GenBank/DBJ databases.
RL  Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RA  Blum H., Baerachis S., Mewes H.-W., Weil B., Wiemann S.;
RL  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.

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```

RC  TISSUE=Brain;
RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
RA  Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko I., Boulford G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
RA  Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -1- FUNCTION: Intrinsic membrane protein of small synaptic
CC  vesicles. Probable vesicular channel protein (By similarity).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
CC  vesicles (By similarity).
CC  -1- SIMILARITY: Belongs to the synaptophysin/synaptobrevin family.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF411860; AAN03681.2; -
DR  EMBL: AL834457; CA039117.1; -
DR  EMBL: BC022518; AAH22518.1; -
DR  Genew; HGNC:16507; SYNPR.
DR  InterPro: IPR008253; Marvel.
DR  InterPro: IPR001285; Synaptophysin.
DR  Pfam: PF01284; MARVEL; 1.
DR  PRINTS: PR00220; SYNAPTOPHYSN.
DR  PROSITE: PS00604; SYNAPTOP; 1.
KM  Synapse; Transmembrane; Synaptosome; Glycoprotein; Repeat.
FT  DOMAIN 1 4
FT  TRANSSEM 5 25
FT  DOMAIN 26 81
FT  TRANSSEM 82 102
FT  DOMAIN 103 114
FT  TRANSSEM 115 135
FT  DOMAIN 136 177
FT  TRANSSEM 178 198
FT  DOMAIN 199 265
FT  DOMAIN 210 242
FT  REPEAT 210 214
FT  REPEAT 214 216
FT  REPEAT 222 226
FT  REPEAT 227 231
FT  REPEAT 232 236
FT  REPEAT 238 242
FT  CARBOHYD 33 33
FT  CARBOHYD 38 38
SQ  SEQUENCE 265 AA; 29166 MW; 2A9DEB870A70F947 CRC64;

Query Match 8.6%; Score 103; DB 1; Length 265;
Best Local Similarity 21.4%; Pred. No. 0.035;
Matches 43; Conservative 39; Mismatches 77; Indels 42; Gaps 10;

QY 53 ESKQMYCVFNREDACRYGSAIGVLAFLVVDAYVFPQSNATDRKLYVIGDLFLS 112
DB 64 KERQKALIGDSSSAEFLVAVFAFLVSLATVYIIFQNKYRKNRPFLI--DRIYV 121

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OY	113	ALTFPELWVGCGFLTNQVA-----VTNPKDVLV-----GACSVR	146
Db	122	VVFSEFLWLVG----SSAWAKSLSDVKATADTKREYLLMSACKOPSNKCMATHSPWSSLN	177
OY	147	AATFSPFSISIKGYGLASLAYORIKAGVDITQNV-DPTDEPNTATASYGASVDNY-Q	204
Db	178	TTSVFFGFNFILMA--GNIVFVFKETGMHSSGQRYSIDPMKEHSSSY-NQGYNODSYGS	234
OY	205	QPFTQNAE---TTE--GYCP	220
Db	235	SSGYSQQASKLGPTSDEFQCP	255

RESULT 12

ID	SYNP_RAT	STANDARD:	PRT,	265 AA.
AC	P22631; Q9ERH1;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Synaptoporin.			
EN	SYNR.			
OS	Rattus norvegicus (rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=91006677; PubMed=2206533;			
RA	Knaus P., Marquese-Pouey B., Scherer H., Betz H.;			
RT	"Synaptoporin, a novel putative channel protein of synaptic vesicles.";			
RL	Neuron 5:453-462(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Dorsal root ganglion;			
RA	Xiao H., Huang Q., Zhang F., Yang Z., Chen Z., Han Z., Zhang X.;			
RL	"Novel genes expressed in rat dorsal root ganglion.";			
CC	Submitted (SEP-2000) to the EMBL/genbank/DBJ databases.			
CC	- FUNCTION: Intrinsic membrane protein of small synaptic vesicles. Probable vesicular channel protein.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic vesicles.			
CC	- TISSUE SPECIFICITY: Central nervous system.			
CC	- SIMILARITY: Belongs to the synaptophysin/synaptobrevin family.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF306459; AAG3231.1; ..			
DR	PIR; JH0300; JH0300.			
DR	InterPro; IPR008253; Marvel.			
DR	InterPro; IPR001285; Synaptophysin.			
DR	Pfam; PF001284; MARVEL; 1.			
DR	PRINTS; PR00220; SYNAPTOPHSN.			
DR	PROSITE; PS00604; SYNAPROP; 1.			
KM	Synapsin, Transmembrane; Synaposome; Glycoprotein; Repeat; Phosphorylation.			
KM	Phosphorylation.			
FT	DOMAIN	1	4	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	5	25	POTENTIAL.
FT	DOMAIN	26	81	VESICULAR (POTENTIAL).
FT	TRANSMEM	82	102	POTENTIAL.
FT	DOMAIN	103	114	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	115	135	POTENTIAL.
FT	DOMAIN	136	177	VESICULAR (POTENTIAL).
FT	TRANSMEM	178	198	POTENTIAL.
FT	DOMAIN	199	265	CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	210	242	1	5 X APPROXIMATE REPEATS.
FT	REPEAT	210	214	1.	
FT	REPEAT	222	226	2.	
FT	REPEAT	227	231	3.	
FT	REPEAT	232	236	4.	
FT	REPEAT	238	242	5.	
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	38	38	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	MOD_RES	212	212	PHOSPHORYLATION (POTENTIAL)	
FT	MOD_RES	220	220	PHOSPHORYLATION (POTENTIAL)	
FT	CONFLICT	68	69	KL -> NV (IN REF. 1)	
FT	CONFLICT	167	167	A -> G (IN REF. 1)	
FT	SEQUENCE	265 AA;	29107 MM;	P12BD8B79F1A28 CRC64;	
QY	Query Match	8.5%;	Score 101;	DB 1;	Length 265;
Db	Best Local Similarity	19.9%;	Pred. No. 0.053;		
Matches	36;	Conservative	36;	Mismatches	73;
				Indels	44;
				Gaps	7;
QY	53	ESKQMCVFNRENEDACRYGSAIGVLAFLASAFVLVDVAFYFQISNATDRKVLVIGDLIFS	112		
Db	64	KERKALVGDSSSAFFPTVAVALFVLLSLAAVYVYIFQNKRRNRRGLI--DRIIV	121		
QY	113	ALMTFLVFGVCFITNQW-----VTNPKDVLV-----GADSVR	146		
Db	122	VVFSEFLVVG-----SSAMAKGLSPVKVATPKFETLMSACKOPSNKCMVHSPVMSLN	177		
QY	147	AAIFSEFISFMSGVLASVYORKAGVDVDFIQVYVDPTDPDPTNPAVSPGASVDYVQCP	206		
Db	178	TSVVFGLNFIPLMA--GNIFVFRFETWHSSGGRYLS---DPMKHS-----SYNG	225		
QY	207	PFTQNAETTEG	217		
Db	226	GYNQDSYSSG	236		

RESULT 13

SYNP\_MOUSE STANDARD; PRT; 265 AA.

ID SYNP\_MOUSE Q8C5U4; Q9DB89;

AC Q8BGN8; Q8C5U4; Q9DB89;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Synaploporin.

GN SYNP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

XX [1]

RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RP STRAIN=C57BL/6J;

RC TISSUE=Cerebellum; Olfactory organ, and Spinal cord;

RC MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi Y., Bono H., Kondo S., Naito I., Otsu N., Saito R., Suzuki H., Yamana K., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gotohori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schirral L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brutsis V., Chochia C., Corbani L.E., Cousins S., Datta E., Dargatz T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J., Grimmond T., Gueirboldi M., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L., Kanaie A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagasima T., Nmatas K., Okido T., Pavan W.J., Petrea G., Pesole G., Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sanderlin A., Schneider C., Sempke C., Setou M., Shimada K., Sultana R., Takenata Y., Taylor M.S., Teasdale R.D., Tomita M., Varadero R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wysshaw-Boris A., Yangisawa M., Yang I., Yang L.,

RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carrini P., Hayatsu N.,  
RA Hirozono-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Niwa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imocant K., Ishii Y., Itoh M., Kaga A.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yamunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs,"  
RL Nature 420:563-573(2002).  
RN [2].  
RN SEQUENCE FROM N.A. (ISOFORM 2).  
RP TISSUE=Dye;  
RC MEDLINE=22388257; PubMed=12477932;  
RX Klausner R.D., Collins F.S., Wagner L., Shem C.M., Schuler G.D.,  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heile F.,  
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stempelen M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrini P., Prange C.,  
RA Bock S.S., Loughanello N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Roak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunarrane P.H.,  
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hailton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,  
RA Schmeich A., Schein J.E., Jones S.J.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Intrinsic membrane protein of small synaptic  
CC vesicles. Probable vesicular channel protein (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic  
CC vesicles (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named Isoforms=2;  
CC Name=1;  
CC IsoId=QB8GN8-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=QB8GN8-1; Sequence=VSP\_008550;  
CC -1- SIMILARITY: Belongs to the synaptophysin/synaptobrevin family.  
CC -----  
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CC -----  
DR EMBL; AK005132; BAB23831.1; -  
DR EMBL; AK032442; BAC27871.1; -  
DR EMBL; AK049661; BAC33864.1; -  
DR EMBL; AK078223; BAC37181.1; -  
DR EMBL; BC026512; AAH26512.1; -  
DR MGD; MGI:1919253; Symp.  
DR InterPro; IPR008253; Marvel.  
DR InterPro; IPR001285; Synaptophysin.  
DR Pfam; PFO1284; MARVEL; 1.  
DR PRINTS; P800604; SYNAPTOPHYS.  
DR PROSITE; PS00604; SYNAPTOPHYS.  
DR Synape; Transmembrane; Synaptosome, Glycoprotein; Repeat;  
KW Alternative splicing.  
FT DOMAIN 1  
FT TRANSMEM 4  
FT TRANSMEM 25  
FT DOMAIN 26  
FT TRANSMEM 81  
FT TRANSMEM 82  
FT DOMAIN 103  
FT TRANSMEM 102  
FT TRANSMEM 103  
FT TRANSMEM 114  
FT TRANSMEM 115  
FT TRANSMEM 135  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.  
FT VESICULAR (POTENTIAL).  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.

Query Match	Best Local Similarity	Matches	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB
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DR EMBL; M22967; AAA30767.1; ALT\_INIT.  
 DR InterPro; IPR008253; Marvel.  
 DR InterPro; IPR001285; Synaptophysin.  
 DR Pfam; PF01284; MARVEL\_1.  
 DR PRINTS; PR00220; SYNAPTOPHYSN.  
 DR PROSITE; PS00604; SYNAPTOP; 1.  
 KM Calcium-binding; Synapse; Glycoprotein; Transmembrane;  
 KM Nerve; Synaptosome; Repeat.  
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 26 49 POTENTIAL.  
 FT DOMAIN 50 106 VESICULAR (POTENTIAL).  
 FT TRANSMEM 107 130 POTENTIAL.  
 FT DOMAIN 131 137 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 138 161 POTENTIAL.  
 FT TRANSMEM 162 199 VESICULAR (POTENTIAL).  
 FT TRANSMEM 200 223 POTENTIAL.  
 FT DOMAIN 224 313 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 314 304 REPEATS; GLY/TVR-RICH.  
 FT CARBOHYD 53 59 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 99 99 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 313 AA; 33910 MW; 3D787D428304587 CRC64;

Query Match 7.9%; Score 94.5; DB 1; Length 313;  
 Best Local Similarity 19.8%; Pred. No. 0.25;  
 Matches 56; Conservative 46; Mismatches 98; Indels 91; Gaps 16;

QY 11 AGGFDLRRLTQPVAVAVCLVFAIVS-----C----- 42  
 DB 15 AGGQF--RVKKEPLGVKVLQWVAFIFATGSGYSGLQLSDVANKTKSDLNIEVF 71  
 QY 43 -----IYGEQYNAHESKQYCVENRNEACRGSAIGVLAFLASAFLLVDAVFQ 94  
 DB 72 EYPRRLHEVFEAPTCQGDPKKIFIVGNYSASA-EFFVVAVAFLYSMALATYIFLGN 130  
 QY 95 ISNATDKYVIGDLFLFSALMTPLMEVGFCLTNQMA-----VTNPKDVLVVG----- 141  
 DB 131 KYRENKGMPL--DFLATAVFAFMVWVS-----SSANAKGSDVKRAKTDENIKGNVCH 184  
 QY 142 -----ADSVRAITSFSPSIFSMGVLAISAYQRYKAG-VDDPIQ---NYVDP 184  
 DB 185 QPQNTCKELDPYTGSGTNTSVVGFGLNLVLM--VGNLMFVKETGMNAAPFLRAPGAPRK 242  
 QY 185 TPEDNTAY--ASY---DG--ASYDNY-----QQPFTQNAET-TEGYQPPPVY 224  
 DB 243 QPAPGDAYGQAGYGGQGGYGPQDSYGPQGGYQPDYGPASGGGGYGPQGDY 295  
 RESULT 15  
 CLF4\_MOUSE STANDARD; PRT; 208 AA.  
 AC Q8JC61; Q8K143;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Chemokine-like factor super family member 4.  
 GN CKLF4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Specific;  
 RA Han W., Ding F., Wang L., Wang Y., Qiu X., Chen Y., Tan Y., Song Q.,  
 Zhang Y., Ma D.;

RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan K., Moore T., Max S.T., Wang Y., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,  
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Mullany S.J.,  
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Scherren A., Schein J.B., Jones S.J.M., Maira M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the chemokine-like factor family.

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Query Match 7.3%; Score 87; DB 1; Length 208;  
 Best Local Similarity 26.7%; Pred. No. 0.74;  
 Matches 46; Conservative 22; Mismatches 56; Indels 48; Gaps 10;

QY 33 LVFALIVFSCIYGEYSNAHESKQY-----CVENRNEACRGSAIGVLAFLASAFLL 86  
 DB 62 VILALIAFICI--ETIMCSPCEGLYFEFEVSC-----SAFVYGVLLILFSL 107  
 QY 87 VVDNAPFOIS-NATDKRYLVIGDLFLFSALMTPLMEVGFCLTNQMAATNPKDVLVGDV 145  
 DB 108 NIMRAIPQINMLT-----DIVNTGLSTFFEFISIVL---AALNKH---TGAEI- 151  
 QY 146 RAATFSFSPSIFSMGVLAISAYQRYKAGV-----DDPIQ---NYVDPTD 187  
 DB 152 -AAVIFGLATAVAVASFTLMQKRVSVRQOSTNDYIRATBSRDVDSRDE 202

Search completed: April 7, 2004, 11:56:50  
 Job time : 19 secs







QY 781 TTCCCATCAGCCCTCTGGAATGCGACCCCTCTCTTCACTGTTCCATCTCTGTGACG 840  
 Db 781 TTCCCATCAGCCCTCTGGAATGCGACCCCTCTCTTCACTGTTCCATCTCTGTGACG 840  
 QY 841 TGAACACAGACTAAGAGAGCTCTAATAGCTGCGGGGCTGCGAGAGCCACACCCCAAGT 900  
 Db 841 TGAACACAGACTAAGAGAGCTCTAATAGCTGCGGGGCTGCGAGAGCCACACCCCAAGT 900  
 QY 901 CCGTGTGCGGAGAGGCTTCACTGAGCCGCTCACTCTCTCCAGGGCACTTTTAGAAAGGT 960  
 Db 901 CCGTGTGCGGAGAGGCTTCACTGAGCCGCTCACTCTCTCCAGGGCACTTTTAGAAAGGT 960  
 QY 961 TTTTAGTAGTGTGTTTCTCTGCTTTTAAATGACCTAGCCCGCTGAGTGGCTGAAG 1020  
 Db 961 TTTTAGTAGTGTGTTTCTCTGCTTTTAAATGACCTAGCCCGCTGAGTGGCTGAAG 1020  
 QY 1021 CAGACAGGTCCCATGTGCTACTGACAGTGTCTGAGCTTCCCGCCGCGGCTGAGG 1080  
 Db 1021 CAGACAGGTCCCATGTGCTACTGACAGTGTCTGAGCTTCCCGCCGCGGCTGAGG 1080  
 QY 1081 CAGGAGAGCCGCTATATCTGCGTCTCTGCGCAAGACTGCTGAGGGCCATGACACTG 1140  
 Db 1081 CAGGAGAGCCGCTATATCTGCGTCTCTGCGCAAGACTGCTGAGGGCCATGACACTG 1140  
 QY 1141 CCGTGTGAGGAGAGCCGAGACAGGCTCTGTGTCTCTCACTGAGTGTGCTTCCCTG 1200  
 Db 1141 CCGTGTGAGGAGAGCCGAGACAGGCTCTGTGTCTCTCACTGAGTGTGCTTCCCTG 1200  
 QY 1201 CCGTGTGAGTATCTGCGGGGCGACACACCTGCTGCGGTGCGCTGAGGCTGCTCCG 1260  
 Db 1201 CCGTGTGAGTATCTGCGGGGCGACACACCTGCTGCGGTGCGCTGAGGCTGCTCCG 1260  
 QY 1261 TGGTGTGAGGAGCGGCGCTGTGTCTCAATGACACTTCTCTGCTGCTCCACCCCGGAG 1320  
 Db 1261 TGGTGTGAGGAGCGGCGCTGTGTCTCAATGACACTTCTCTGCTGCTCCACCCCGGAG 1320  
 QY 1321 GGAAGAGGCTTTCCTGACACACCCAGCTTATGTAATATTTCTCACTGTTACTTNG 1380  
 Db 1321 GGAAGAGGCTTTCCTGACACACCCAGCTTATGTAATATTTCTCACTGTTACTTNG 1380  
 QY 1381 GGAAGAGGCTTTCCTGACACACCCAGCTTATGTAATATTTCTCACTGTTACTTNG 1440  
 Db 1381 GGAAGAGGCTTTCCTGACACACCCAGCTTATGTAATATTTCTCACTGTTACTTNG 1440  
 QY 1441 TATTAATCTGTGGGAGATGCGCGCTGTGGATGCTGTTTGGAGACGGAATTAATGTTT 1500  
 Db 1441 TATTAATCTGTGGGAGATGCGCGCTGTGGATGCTGTTTGGAGACGGAATTAATGTTT 1500  
 QY 1501 TCTCATTAAG 1512  
 Db 1501 TCTCATTAAG 1512

RESULT 2  
 AAC78493  
 ID AAC78493 standard; cDNA; 1512 BP.  
 AC AAC78493;  
 DT 08-FEB-2001 (first entry)

XX Human PRO615 (UNQ352) nucleotide sequence SEQ ID NO:161.  
 XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 XX expressed sequence tag; detection; cancer; ss.  
 OS Homo sapiens.  
 FN W0200053756-A2.  
 PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US004341.  
 XX 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 29-MAR-1999; 99US-0126773P.  
 PR 21-APR-1999; 99US-0130232P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Boctstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Filvaroli E, Fong S, Gao W, Gerber H, Gertlisen ME,  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
 PI K1avian J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX MPI, 2000-611443/58.  
 DR P-FSDB; AAB44265.  
 XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 PS Claim 2; Fig 60; 636pp; English.  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytosolic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences  
 XX Sequence 1512 BP; 246 A; 482 C; 446 G; 338 T; 0 U; 0 Other;  
 QY Query Match 100.0%; Score 1512; DB 3; Length 1512;  
 QY Best Local Similarity 100.0%; Pred. No. 0;  
 Db Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGAAGCGGTGGGAGAGCGCGGTGGGCGGCGGAGCGGCGGAGCATGAGAGCG 60  
 Db 1 CGAAGCGGTGGGAGAGCGCGGTGGGCGGCGGAGCGGCGGAGCATGAGAGCG 60  
 QY 61 GGGCTTAAGCGGCGGCGGAGAGCGGCGGCTCTTGAAGCTGCGGCGCTTCTGAAGC 120  
 Db 61 GGGCTTAAGCGGCGGCGGAGAGCGGCGGCTCTTGAAGCTGCGGCGCTTCTGAAGC 120  
 QY 121 CGAGAGTGTGGGCGGCGGCGGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 180  
 Db 121 CGAGAGTGTGGGCGGCGGCGGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 180  
 QY 181 ATGTGAAGGCTACAGCAATGCGGAGCTTGAAGAGATGATGCTGCTTGAAGCGCA 240  
 Db 181 ATGTGAAGGCTACAGCAATGCGGAGCTTGAAGAGATGATGCTGCTTGAAGCGCA 240  
 QY 241 ACGAGATGCTGCGGCTATGAGAGTGCATCGGGGTGTGCGCTTCTGCGCT 300

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Db      241  ACGAGAGTCTGCGGCTATGGAGTGCATCGGGGTCTGGCTTCTGGCTCGGCT 300
Qy      301  TCTTCTGGTGGTGCAGCGGTATTTCCCCAGATGACACAGCACTGACCGCAAGTACC 360
Db      301  TCTTCTGGTGGTGCAGCGGTATTTCCCCAGATGACACAGCACTGACCGCAAGTACC 360
Qy      361  TGGTATGTGAGTGTCTCTTCTGAGTCTGTGACCTTCTGAGTTGTGTTTCT 420
Db      361  TGGTATGTGAGTGTCTCTTCTGAGTCTGTGACCTTCTGAGTTGTGTTTCT 420
Qy      421  GCTTCTCAACCAACAGTGGGAGTCAACACCCGAGAGAGTGTGTGGGGCCGACT 480
Db      421  GCTTCTCAACCAACAGTGGGAGTCAACACCCGAGAGAGTGTGTGGGGCCGACT 480
Qy      481  CTGTAGGGGAGGAGTCACTGAGTCTTCTTCTGATCTTCTGAGGAGTGTGAGCT 540
Db      481  CTGTAGGGGAGGAGTCACTGAGTCTTCTTCTGATCTTCTGAGGAGTGTGAGCT 540
Qy      541  CCTTGGCTTACCGAGCGCTACAGAGCTGGCGTGAAGCACTTCAACCAATTACGTTGACC 600
Db      541  CCTTGGCTTACCGAGCGCTACAGAGCTGGCGTGAAGCACTTCAACCAATTACGTTGACC 600
Qy      601  CCATCTCCGAGCCCAACCACTGCTTACGCTCTCTTACCCAGTGCATCTGTGACAACTACC 660
Db      601  CCATCTCCGAGCCCAACCACTGCTTACGCTCTCTTACCCAGTGCATCTGTGACAACTACC 660
Qy      661  AACAGCCACCTTCAACCCAGAGGAGAGACCAACGAGGAGTACAGCCGCGCCCTGTGT 720
Db      661  AACAGCCACCTTCAACCCAGAGGAGAGACCAACGAGGAGTACAGCCGCGCCCTGTGT 720
Qy      721  ACTGAGTGGCGGTTAGCGTGGAGAGGGGAGACAGAGAGGAGGCTTCCCTCTGCGCTGAGT 780
Db      721  ACTGAGTGGCGGTTAGCGTGGAGAGGGGAGACAGAGAGGAGGCTTCCCTCTGCGCTGAGT 780
Qy      781  TTCCCATCAGGCTCTCTGAACTGCGAGGCGCTCTTCTTCACTGTCATCTGTGAGC 840
Db      781  TTCCCATCAGGCTCTCTGAACTGCGAGGCGCTCTTCTTCACTGTCATCTGTGAGC 840
Qy      841  TGACACACAGCTAAGAGAGCTCTCATAGCTGGCGGGGCTGGCAGAGCCACCCCAAGTG 900
Db      841  TGACACACAGCTAAGAGAGCTCTCATAGCTGGCGGGGCTGGCAGAGCCACCCCAAGTG 900
Qy      901  CCTGAGCCAGAGGAGCTTCAAGTCAAGCGGCTCACTCTTCAAGGAGCACTTTTGAAGAGGT 960
Db      901  CCTGAGCCAGAGGAGCTTCAAGTCAAGCGGCTCACTCTTCAAGGAGCACTTTTGAAGAGGT 960
Qy      961  TTTTAGCTAGTGTCTTCTGCTTCTTATGACCTGACCCCGCTGAGTGTGAGT 1020
Db      961  TTTTAGCTAGTGTCTTCTGCTTCTTATGACCTGACCCCGCTGAGTGTGAGT 1020
Qy      1021  CCAGAGAGTGGCCATGATCTGACAGTGCCTGAGTCTTCCCGCGCGCGGCTGAGG 1080
Db      1021  CCAGAGAGTGGCCATGATCTGACAGTGCCTGAGTCTTCCCGCGCGCGGCTGAGG 1080
Qy      1081  CGTGGAGCGGCTATATCTGCTTCTGCAAGAGCTCGTGGGGGCAATCACACCTGC 1140
Db      1081  CGTGGAGCGGCTATATCTGCTTCTGCAAGAGCTCGTGGGGGCAATCACACCTGC 1140
Qy      1141  CCTGTGAGGAGGAGCGGAGCCAGAGTCTTGTGCTCTCAAGTGTGCTTCCCTGTC 1200
Db      1141  CCTGTGAGGAGGAGCGGAGCCAGAGTCTTGTGCTCTCAAGTGTGCTTCCCTGTC 1200
Qy      1201  CCACGCTGTATGATCTGTGGGAGCACCAACCTGTGCGCGGTCTGGGCTGCTCCG 1260
Db      1201  CCACGCTGTATGATCTGTGGGAGCACCAACCTGTGCGCGGTCTGGGCTGCTCCG 1260
Qy      1261  TGGTGTGAGGAGGAGGAGTGTGCTATAGCACTTCTCTGCTTCCACCCCTGGAGCA 1320
Db      1261  TGGTGTGAGGAGGAGGAGTGTGCTATAGCACTTCTCTGCTTCCACCCCTGGAGCA 1320
Qy      1321  GGGAGAGGCTTGTGCTGACCAACCCAGCTTATATTAATTTCTGAGTGTACTTAG 1380

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Db      1321  GGGAGAGGCTTGTGCTGACCAACCCAGCTTATATTAATTTCTGAGTGTACTTAG 1380
Qy      1381  GAAAGCTGGGAGAGGAGGAGGTGCCCCATGCTCCCAAGCTGTGCTGTGCGAGTGTAT 1440
Db      1381  GAAAGCTGGGAGAGGAGGAGGTGCCCCATGCTCCCAAGCTGTGCTGTGCGAGTGTAT 1440
Qy      1441  TATTAATCGTGGGAGAGTCCCGGCTGGAGTCTGTTTGAAGAGCAATTAATGTTT 1500
Db      1441  TATTAATCGTGGGAGAGTCCCGGCTGGAGTCTGTTTGAAGAGCAATTAATGTTT 1500
Qy      1501  TCTCATTAAG 1512
Db      1501  TCTCATTAAG 1512

RESULT 3
AAC58232
ID AAC58232 standard; cDNA; 1512 BP.
XX
AC AAC58232;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO615 nucleotide sequence SEQ ID NO:15.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
KW tumorigenesis; detection; neoplastic cell growth; proliferation;
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
KW immunological disorder; ss.
XX
OS Homo sapiens.
XX
EN WO200053754-A1.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000277.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-013445P.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
PI Wood WI;
XX
DR P-PDSB; AAB24048.
XX
PT New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment.
XX
PS Claim 50; Fig 15; 195pp; English.
XX
CC The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO327, PRO324, PRO351, PRO362, PRO615, PRO531, PRO364, PRO618,
CC PRO372, PRO703, PRO792 or PRO474. The Ab can be used in compositions and
CC methods for the diagnosis and treatment of neoplastic cell growth and
CC proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumour cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumour treatment. Compounds

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CC that inhibit the expression or activity of the identified polypeptides  
 CC can be identified and used as antagonists. Benign or malignant tumours,  
 CC inflammatory disorders and immunological disorders can be treated.  
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
 CC AAC24041 to AAC24056 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention  
 XX

Sequence 1512 BP; 246 A; 482 C; 446 G; 338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1512; DB 3; Length 1512;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGGAGCGCTGGGCGGACCGCTGGGGCGGCGGACCGGCGGCGGAGCGGACATGGAGCG 60
DB 1 CGGAGCGCTGGGCGGACCGCTGGGGCGGCGGACCGGCGGCGGAGCGGACATGGAGCG 60
QY 61 GGGGCTACGGGCGGCGGCGGAGCGGCGGCGCTCTTGAAGCTTGGGCGCTTCTGACGAGC 120
DB 61 GGGGCTACGGGCGGCGGCGGAGCGGCGGCGCTCTTGAAGCTTGGGCGCTTCTGACGAGC 120
QY 121 CGGAGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CGGAGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
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QY 301 TCTTCTTGGTGGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 301 TCTTCTTGGTGGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
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DB 361 TGGGATGTTGAGCTGCTCTTCAAGCTCTTGAAGCTTCTGAGGTTGTTGTTTCT 420
QY 421 GCTTCTTCAACCAACAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 421 GCTTCTTCAACCAACAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 481 CTGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
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DB 601 CCAATCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 AACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
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QY 841 TGAACACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
DB 841 TGAACACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900

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QY 901 CCTGTGCCAGAGGCGGCTTCACTCAGCCGCTCACTCCGCAAGGCACTTTAGAAAGGT 960
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QY 961 TTTTACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 TTTTACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1021 CCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
DB 1021 CCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
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QY 1501 TCTCATTTCAAAG 1512
DB 1501 TCTCATTTCAAAG 1512

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RESULT 4  
 ACD42560  
 ID ACD42560 standard; cDNA, 1512 BP.  
 XX  
 AC ACD42560;  
 XX  
 DT 09-SEP-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO615 cDNA.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;  
 KW cell death; growth induction cascade; blood coagulation cascade;  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003050239-A1.  
 PD 13-MAR-2003.  
 XX  
 PF 15-OCT-2001; 2001US-00978191.  
 XX  
 PR 17-OCT-1997; 97US-0062250P.  
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PR 02-NOV-1998; 98US-00184216.  
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PR 08-MAR-1999; 98US-00255028.  
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PR 12-MAR-1999; 98US-00267213.  
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PR 05-JAN-2000; 2000US-0000219.  
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PR 21-MAR-2000; 2000US-00075532.  
PR 30-MAR-2000; 2000US-0008435.  
PR 17-MAY-2000; 2000US-0013705.  
PR 22-MAY-2000; 2000US-0014042.  
PR 30-MAY-2000; 2000US-0014941.



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XX
DE Novel human secreted and transmembrane protein PRO615 cDNA.
XX
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
XX antiarteriosclerotic; cardiant; anti-inferility; anti-HIV; cytoskeletal;
XX antidiabetic; gene therapy; inflammatory disease; organ failure;
XX atherosclerosis; cardiac injury; infertility; birth defect;
XX premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
XX gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
XX tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
XX US2002192706-A1.
XX
XX 19-DEC-2002.
XX
XX 24-OCT-2001; 2001US-00999832.
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XX 17-OCT-1997; 97US-00622502.
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XX PR 20-NOV-1998; 98WO-US024855.
XX PR 05-JAN-1999; 99WO-US000106.
XX PR 08-MAR-1999; 99WO-US005028.

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PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
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PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000217.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 30-MAR-2000; 2000WO-US007532.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034955.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 28-JUN-2001; 2001WO-US021065.
PR 03-JUL-2001; 2001WO-US021735.

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## (GETH) GENENTECH INC.

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XX Ahkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerltsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan RJ;
XX Kijavrin IJ, Kuo SS, Napier MA, Pan J, Pont NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WT;
XX WPI; 2003-328660/31.
XX DR P-PSDB; AB072217.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
XX as PRO, useful for treating inflammation, organ failure, atherosclerosis,
XX cardiac injury, infertility, birth defects, premature aging, AIDS, or
XX cancer.
XX
XX Claim 2; Fig 60; 453pp; English.

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The invention describes an isolated nucleic acid (i) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridization probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 1512 BP; 246 A; 482 C; 446 G; 338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1512; DB 7; Length 1512;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db	1061	CGTGGAGCCCTATTATCTGCGTTCTTGCCAAAGACTGATGGAGGCATACACCTTGC	1140
Qy	1141	CGTGTGACGGAGACCCGAGCCAGGCTCTTGTCCTCACTCAGGTTTGCCTCCCTGTGC	1200
Db	1141	CCTGTGACGGAGACCCGAGCCAGGCTCTTGTCCTCACTCAGGTTTGCCTCCCTGTGC	1200
Qy	1201	CCACTGCTGTATATATCTGGGGGCCACCAACCTGTGCGGATGGCCTCTTGAGCTGCTCCG	1260
Db	1201	CCACTGCTGTATATATCTGGGGGCCACCAACCTGTGCGGATGGCCTCTTGAGCTGCTCCG	1260
Qy	1261	TGTTGTGAGGGCGGGGCGTGTGCTCATGAGCACTTCTCTTGCTCCACCCCTGGACGA	1320
Db	1261	TGTTGTGAGGGCGGGGCGTGTGCTCATGAGCACTTCTCTTGCTCCACCCCTGGACGA	1320
Qy	1321	GGGAAAGGCTTTGGCTTGACAAACCCAGCTTATATATAATTTGTGAGTTGTTACTTAG	1380
Db	1321	GGGAAAGGCTTTGGCTTGACAAACCCAGCTTATATATAATTTGTGAGTTGTTACTTAG	1380
Qy	1381	GAAAGCTGGAGGAGGAGGGGTGGCCCATGGGCTCCAGACCTGTCTGTGCGGAGTGTAT	1440
Db	1381	GAAAGCTGGAGGAGGAGGGGTGGCCCATGGGCTCCAGACCTGTCTGTGCGGAGTGTAT	1440
Qy	1441	TATATAATCGTGGGGAGATATGCCCGGCTGGAGTGTCTTTGGAGACGAAATAATGTTT	1500
Db	1441	TATATAATCGTGGGGAGATATGCCCGGCTGGAGTGTCTTTGGAGACGAAATAATGTTT	1500
Qy	1501	TCTCATTCGAAG 1512	
Db	1501	TCTCATTCGAAG 1512	
RESULT 6			
ACA71759			
ID	ACA71759	standard; cDNA; 1512 BP.	
AC	ACA71759;		
AC	ACA71759;		
XX	11-AUG-2003	(first entry)	
XX			
DE	Human secreted and transmembrane polypeptide PRO615 cDNA.		
KM	Human; sex; gene; thrombolytic agent; interferon; interleukin; cytokine;		
KM	erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;		
KM	apoptosis related condition; AIDS; amyotrophic lateral sclerosis;		
KM	inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;		
KM	gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;		
KM	hypertension; myocardial ischaemia; kidney disease; carcinogenesis;		
KM	glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;		
KM	bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;		
KM	inflammatory bowel disease; reproductive disorder; premature labour.		
XX			
OS	Homo sapiens.		
XX			
PN	US2002177553-A1.		
XX			
PD	28-NOV-2002.		
XX			
PF	15-OCT-2001; 2001US-00978192.		
XX			
PR	17-OCT-1997; 97US-0062250P.		
PR	03-NOV-1997; 97US-0064249P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	21-NOV-1997; 97US-0066354P.		
PR	10-MAR-1998; 98US-0077450P.		
PR	11-MAR-1998; 98US-0077632P.		
PR	11-MAR-1998; 98US-0077641P.		
PR	11-MAR-1998; 98US-0077649P.		
PR	12-MAR-1998; 98US-0077791P.		
PR	13-MAR-1998; 98US-0078004P.		
PR	17-MAR-1998; 98US-00040220.		
PR	20-MAR-1998; 98US-0078886P.		
PR	20-MAR-1998; 98US-0078910P.		









QY 781 TTCCATCAGGCTCTCTGAACTGCGAGCCCTCTCTTCACTGTCATCTGTGAGC 840  
Db 781 TTCCATCAGGCTCTCTGAACTGCGAGCCCTCTCTTCACTGTCATCTGTGAGC 840  
QY 841 TGAACACAGTATAGAGCCCTCATAGCTGCGGGGGCTGCGAGGCCACACCCCAAGT 900  
Db 841 TGAACACAGTATAGAGCCCTCATAGCTGCGGGGGCTGCGAGGCCACACCCCAAGT 900  
QY 901 CCTGTGCCAGAGGGCTTCACTGAGCCGCTCACTCTCCAGAGGACATTTAGAAAGGT 960  
Db 901 CCTGTGCCAGAGGGCTTCACTGAGCCGCTCACTCTCCAGAGGACATTTAGAAAGGT 960  
QY 961 TTTTAGCTAGTGTCTTCTCTGCTTTTAATGACCTGAGCCCGCTGAGTGAAG 1020  
Db 961 TTTTAGCTAGTGTCTTCTCTGCTTTTAATGACCTGAGCCCGCTGAGTGAAG 1020  
QY 1021 CCAGCAGGTGCGCATGCTACTGACAAAGTCCCTGAGCTTCCCGCGCGCGGCTAGAGC 1080  
Db 1021 CCAGCAGGTGCGCATGCTACTGACAAAGTCCCTGAGCTTCCCGCGCGGCTAGAGC 1080  
QY 1081 CTGTGGAGCGCTATATCTGCGCTTCTGCGAAAGACTGCGGGGCGATCAACCTGC 1140  
Db 1081 CTGTGGAGCGCTATATCTGCGCTTCTGCGAAAGACTGCGGGGCGATCAACCTGC 1140  
QY 1141 CCTGTGAGGAGGAGCGGACCGGACCGAGCTTGTGCTCTGACTGAGTTGCTTCCCTGTGC 1200  
Db 1141 CCTGTGAGGAGGAGCGGACCGGACCGAGCTTGTGCTCTGACTGAGTTGCTTCCCTGTGC 1200  
QY 1201 CCACCTGCTGATGATCTGCGGGGCGACCACTGCGGGGCGAGTCTGCGGCTGCTCCG 1260  
Db 1201 CCACCTGCTGATGATCTGCGGGGCGACCACTGCGGGGCGAGTCTGCGGCTGCTCCG 1260  
QY 1261 TGGTGTAGGGGCGGGGCTGTGCTGATGACCTTCTGCTCCACCCCTGCGAGCA 1320  
Db 1261 TGGTGTAGGGGCGGGGCTGTGCTGATGACCTTCTGCTCCACCCCTGCGAGCA 1320  
QY 1321 GGGAGAGGCTTTGCTGACAAACCCAGCTTTATGTAATCTGCACTGTTAGTTAG 1380  
Db 1321 GGGAGAGGCTTTGCTGACAAACCCAGCTTTATGTAATCTGCACTGTTAGTTAG 1380  
QY 1381 GAAAGCTGGGAGAGGCGAGGGGTGCCCATGCTCCAGACTCTGTGTGCGAGTAT 1440  
Db 1381 GAAAGCTGGGAGAGGCGAGGGGTGCCCATGCTCCAGACTCTGTGTGCGAGTAT 1440  
QY 1441 TATATAATCGTGGGAGATGCCCGGCTGAGTGTGAGAGCGAATAATGTT 1500  
Db 1441 TATATAATCGTGGGAGATGCCCGGCTGAGTGTGAGAGCGAATAATGTT 1500  
QY 1501 TCTCATTCAAAG 1512  
Db 1501 TCTCATTCAAAG 1512

RESULT 8  
ACA66140  
ID ACA66140 standard, cDNA, 1512 BP.  
XX  
AC ACA66140;  
XX  
DT 24-JUN-2003 (first entry)  
XX  
DE Human cDNA encoding secreted/transmembrane protein PRO615.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
KW malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;  
KW leukemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;  
KW infertility; premature aging; psoriasis; inflammatory disease;  
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;  
KW hepatitis; multiple sclerosis; gene therapy.  
OS Homo sapiens.  
XX

PN US2003004102-A1.  
XX  
PD 02-JAN-2003.  
XX  
PF 15-OCT-2001; 2001US-00978189.  
XX  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 26-JUN-1998; 98US-00105413.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98WO-US021141.  
PR 02-NOV-1998; 98US-00184216.  
PR 06-NOV-1998; 98US-00187368.  
PR 20-NOV-1998; 98WO-US024855.  
PR 07-DEC-1998; 98US-00202054.  
PR 22-DEC-1998; 98US-00218517.  
PR 05-JAN-1999; 98WO-US000106.  
PR 05-JAN-1999; 98US-00254465.  
PR 08-MAR-1999; 98WO-US005028.  
PR 10-MAR-1999; 98US-00265686.  
PR 12-MAR-1999; 98WO-US005190.  
PR 12-APR-1999; 98US-00267213.  
PR 14-MAY-1999; 98US-00284291.  
PR 14-MAY-1999; 98US-00311832.  
PR 02-JUN-1999; 98WO-US010733.  
PR 25-JUN-1999; 98WO-US011252.  
PR 25-AUG-1999; 98US-00380137.  
PR 25-AUG-1999; 98US-00380138.  
PR 30-NOV-1999; 98WO-US028313.  
PR 02-DEC-1999; 98WO-US028551.  
PR 02-DEC-1999; 98WO-US028565.  
PR 16-DEC-1999; 98WO-US030095.  
PR 30-DEC-1999; 98WO-US031243.  
PR 05-JAN-1999; 98WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000377.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.

PR	24-AUG-2000	2001MO-US023328
PR	06-NOV-2000	2001MO-US029928
PR	15-NOV-2000	2001MO-US030875
PR	27-NOV-2000	2001MO-US032748
PR	01-DEC-2000	2001MO-US033678
PR	20-DEC-2000	2001MO-US047259
PR	20-DEC-2000	2001MO-US034956
PR	20-DEC-2000	2001MO-US050620
PR	28-FEB-2001	2001MO-US081574
PR	22-MAR-2001	2001MO-US081620
PR	22-MAR-2001	2001MO-US093552
PR	16-MAY-2001	2001MO-US085208
PR	10-MAY-2001	2001MO-US084280
PR	25-MAY-2001	2001MO-US051092
PR	01-JUN-2001	2001MO-US087035
PR	01-JUN-2001	2001MO-US017800
PR	05-JUN-2001	2001MO-US084503
PR	14-JUN-2001	2001MO-US086536
PR	19-JUN-2001	2001MO-US086342
PR	20-JUN-2001	2001MO-US019692
PR	29-JUN-2001	2001MO-US021066
PR	03-JUL-2001	2001MO-US021735
PR	30-JUL-2001	2001MO-US091585

(GETH ) GENENTECH INC.

Ashkenzi AV, Baker KP, Bornstein D, Deeneyers L, Eaton DL, Ferrara N, Filaretov E, Fong S, Gao W, Gerber H, Gottard A, Godowski P, Grimaldi JC, Gurley AL, Hillan KJ, Klabian J, Kuo SS, Napier MA, Pan Q, Paoni NF, Roy MA, Stewart CA, Thomas D, Williams PM, Wood WI, Shelton DL

WPI; 2003-341189/32.  
P-PSDB; ABU80364.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO155), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 2; Fig 60; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, neurosis, atherosclerosis, infertility, premature aging, psoriasis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

```
Db      961  TTTAGTAGTGTGTTTCTGCTTTATGACCTCAGCCCGGCTGAGTGCTAGAG 1020
Qy      1021  CCAGAGGTGCCCAATGCTCTACTGACAGTGCCTCAGTTCCCGCCGCGGCTCAGGC 1080
Db      1021  CCAGAGGTGCCCAATGCTCTACTGACAGTGCCTCAGTTCCCGCCGCGGCTCAGGC 1080
Qy      1081  CGTGGAGCCCGCTATTTATCTGCTCTGTCGCAAGATCGTGGGCGGCATCAGCTGCG 1140
Db      1081  CGTGGAGCCCGCTATTTATCTGCTCTGTCGCAAGATCGTGGGCGGCATCAGCTGCG 1140
Qy      1141  CCTGTGACGCGGAGCGGACCCAGGCTCTTGTGTCTCTACTAGGTTTCTTCCCTGTC 1200
Db      1141  CCTGTGACGCGGAGCGGACCCAGGCTCTTGTGTCTCTACTAGGTTTCTTCCCTGTC 1200
Qy      1201  CCACGCTGTATGATCTGCGGCGGCACACCCCTGTCGCGGCTGCGGCTGCGCCG 1260
Db      1201  CCACGCTGTATGATCTGCGGCGGCACACCCCTGTCGCGGCTGCGGCTGCGCCG 1260
Qy      1261  TGGTGTGAGGGCGGGGCTGTGTCTATGCACTTCTCTTCCCAACCCCTGGAGCA 1320
Db      1261  TGGTGTGAGGGCGGGGCTGTGTCTATGCACTTCTCTTCCCAACCCCTGGAGCA 1320
Qy      1321  GGGAGGAGCTTGTGCTGCAACACCCAGCTTTATGTAATTTCTGAGTTGTTACTTAG 1380
Db      1321  GGGAGGAGCTTGTGCTGCAACACCCAGCTTTATGTAATTTCTGAGTTGTTACTTAG 1380
Qy      1381  GAAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1440
Db      1381  GAAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1440
Qy      1441  TATTAATCGTGGGAGGAGTCCCGGCTGGGAGTCTGTTGGAGAGGAGTAATGTTT 1500
Db      1441  TATTAATCGTGGGAGGAGTCCCGGCTGGGAGTCTGTTGGAGAGGAGTAATGTTT 1500
Qy      1501  TCTCATTCGAAG 1512
Db      1501  TCTCATTCGAAG 1512

RESULT 9
ADA24700
ID      ADA24700 standard; cDNA; 1512 BP.
XX
AC      ADA24700;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Novel human secreted and transmembrane protein PRO615 cDNA.
XX
KW      Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
KW      chromosome identification; vaccine; cancer; retinal disorder;
KW      sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW      wound healing; obesity; diabetes; hearing loss;
KW      cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW      haemoglobin associated disorder.
XX
OS      Homo sapiens.
XX
PN      US2003050241-A1.
XX
PD      13-MAR-2003.
XX
PF      16-OCT-2001; 2001US-00978564.
XX
PR      17-OCT-1997; 97US-0062250P.
PR      03-NOV-1997; 97US-0064248P.
PR      13-NOV-1997; 97US-0065311P.
PR      21-NOV-1997; 97US-0068364P.
PR      10-MAR-1998; 98US-0077450P.
PR      11-MAR-1998; 98US-0077632P.
PR      11-MAR-1998; 98US-0077641P.
PR      11-MAR-1998; 98US-0077649P.
PR      12-MAR-1998; 98US-0077791P.

PR      13-MAR-1998; 98US-0078004P.
PR      20-MAR-1998; 98US-0078810P.
PR      20-MAR-1998; 98US-0078936P.
PR      20-MAR-1998; 98US-0078939P.
PR      25-MAR-1998; 98US-0079294P.
PR      26-MAR-1998; 98US-0079656P.
PR      27-MAR-1998; 98US-0079663P.
PR      27-MAR-1998; 98US-0079668P.
PR      27-MAR-1998; 98US-0079786P.
PR      30-MAR-1998; 98US-0079923P.
PR      31-MAR-1998; 98US-0080105P.
PR      31-MAR-1998; 98US-0080107P.
PR      31-MAR-1998; 98US-0080165P.
PR      31-MAR-1998; 98US-0080194P.
PR      01-APR-1998; 98US-0080327P.
PR      01-APR-1998; 98US-0080328P.
PR      01-APR-1998; 98US-0080333P.
PR      08-APR-1998; 98US-0080349P.
PR      08-APR-1998; 98US-0081049P.
PR      08-APR-1998; 98US-0081070P.
PR      09-APR-1998; 98US-0081071P.
PR      09-APR-1998; 98US-0081195P.
PR      09-APR-1998; 98US-0081203P.
PR      15-APR-1998; 98US-0081229P.
PR      15-APR-1998; 98US-0081817P.
PR      15-APR-1998; 98US-0081819P.
PR      15-APR-1998; 98US-0081836P.
PR      15-APR-1998; 98US-0081952P.
PR      15-APR-1998; 98US-0081955P.
PR      21-APR-1998; 98US-0082568P.
PR      22-APR-1998; 98US-0082569P.
PR      22-APR-1998; 98US-0082700P.
PR      22-APR-1998; 98US-0082704P.
PR      22-APR-1998; 98US-0082797P.
PR      22-APR-1998; 98US-0082804P.
PR      23-APR-1998; 98US-0082796P.
PR      27-APR-1998; 98US-0083332P.
PR      28-APR-1998; 98US-0083322P.
PR      29-APR-1998; 98US-0083392P.
PR      29-APR-1998; 98US-0083495P.
PR      29-APR-1998; 98US-0083496P.
PR      29-APR-1998; 98US-0083499P.
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PR      29-APR-1998; 98US-0083545P.
PR      29-APR-1998; 98US-0083554P.
PR      29-APR-1998; 98US-0083558P.
PR      29-APR-1998; 98US-0083559P.
PR      30-APR-1998; 98US-0083742P.
PR      05-MAY-1998; 98US-0084366P.
PR      06-MAY-1998; 98US-0084414P.
PR      06-MAY-1998; 98US-0084414P.
PR      07-MAY-1998; 98US-0084598P.
PR      07-MAY-1998; 98US-0084600P.
PR      07-MAY-1998; 98US-0084627P.
PR      07-MAY-1998; 98US-0084637P.
PR      07-MAY-1998; 98US-0084639P.
PR      07-MAY-1998; 98US-0084640P.
PR      07-MAY-1998; 98US-0084643P.
PR      13-MAY-1998; 98US-0085323P.
PR      13-MAY-1998; 98US-0085338P.
PR      13-MAY-1998; 98US-0085339P.
PR      15-MAY-1998; 98US-0085573P.
PR      15-MAY-1998; 98US-0085579P.
PR      15-MAY-1998; 98US-0085800P.
PR      15-MAY-1998; 98US-0085822P.
PR      15-MAY-1998; 98US-0085889P.
PR      15-MAY-1998; 98US-0085897P.
PR      15-MAY-1998; 98US-0085700P.
PR      15-MAY-1998; 98US-0085704P.
```



DB 661 AACAGCCACCTTACCCAGAACCGGAGACACCCGAGGCTACACGCCGCCCTCTGT 720  
 QY 721 ACTGATGGCCGTTAGCGTGGGAAAGGGGACAGAGAGGCCCTCTCCCTTGGCTGACT 760  
 DB 721 ACTGATGGCCGTTAGCGTGGGAAAGGGGACAGAGAGGCCCTCTCCCTTGGCTGACT 760  
 QY 781 TTCCCATCAGCGCTCTGGAATCGACAGGCCCTCTCTTTCACTGTTCATCTCTGTGAGC 840  
 DB 781 TTCCCATCAGCGCTCTGGAATCGACAGGCCCTCTCTTTCACTGTTCATCTCTGTGAGC 840  
 QY 841 TGACACACAGCTTAAGAGACCTCATAGCCTGGCGGGGCTGGACAGACACCCCAAGTG 900  
 DB 841 TGACACACAGCTTAAGAGACCTCATAGCCTGGCGGGGCTGGACAGACACCCCAAGTG 900  
 QY 901 CCGTGGCCAGAGGGCTTCAGTCAAGCGGCTCACTCTCCAGGGGACATTTAGGAAAGGT 960  
 DB 901 CCGTGGCCAGAGGGCTTCAGTCAAGCGGCTCACTCTCCAGGGGACATTTAGGAAAGGT 960  
 QY 961 TTTTAGCTAGTGTCTTCTGCTTTTATGACCTCAGCCCGGCTGAGTGGCTAGAG 1020  
 DB 961 TTTTAGCTAGTGTCTTCTGCTTTTATGACCTCAGCCCGGCTGAGTGGCTAGAG 1020  
 QY 1021 CCAGCAGGTGGCCCATGTGCTCTGACAAAGTCTCAGTTCGCCCGGCGGCTCAGGC 1080  
 DB 1021 CCAGCAGGTGGCCCATGTGCTCTGACAAAGTCTCAGTTCGCCCGGCGGCTCAGGC 1080  
 QY 1081 CGTGGAGCCGCTTATCTGCTCTCTGCAAGAGTCTGAGGGGACATCACACTGC 1140  
 DB 1081 CGTGGAGCCGCTTATCTGCTCTCTGCAAGAGTCTGAGGGGACATCACACTGC 1140  
 QY 1141 CCTGTGACGCGGAGCCGACCAAGGCTCTGTGTCTCTCACTCAGTTCCTCTGCTGC 1200  
 DB 1141 CCTGTGACGCGGAGCCGACCAAGGCTCTGTGTCTCTCACTCAGTTCCTCTGCTGC 1200  
 QY 1201 CCACCTGCTGTATGATCTGAGGGGACCAACCTGTGCGGTGAGCTGAGCTCCG 1260  
 DB 1201 CCACCTGCTGTATGATCTGAGGGGACCAACCTGTGCGGTGAGCTGAGCTCCG 1260  
 QY 1261 TGGTGTGAGGGCGGGGCTGTGCTCATGAGCACTTCTCTGCTCCACCCCTGGCAGCA 1320  
 DB 1261 TGGTGTGAGGGCGGGGCTGTGCTCATGAGCACTTCTCTGCTCCACCCCTGGCAGCA 1320  
 QY 1321 GGGAGAGGCTTGGCTGACACACCCAGCTTATGTAATATCTGAGTGTACTTAG 1380  
 DB 1321 GGGAGAGGCTTGGCTGACACACCCAGCTTATGTAATATCTGAGTGTACTTAG 1380  
 QY 1381 GAAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1440  
 DB 1381 GAAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1440  
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 DB 1441 TATTAATCTGAGGGGAGATGCCCGGCTGGAGTGTGTTGGAGAGGAAATATGTTT 1500  
 QY 1501 TCTCATTCAGAG 1512  
 DB 1501 TCTCATTCAGAG 1512  
 RESULT 10  
 ACD29741  
 ID ACD29741 standard; cDNA, 1512 BP.  
 XX ACD29741;  
 AC 08-SEP-2003 (first entry)  
 XX DT  
 XX Novel human secreted and transmembrane protein PRO615 cDNA.  
 XX DE  
 XX Human; secreted and transmembrane protein; PRO; cell death; neuropathy;  
 KW peripheral neuropathy; diabetic peripheral neuropathy;  
 KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;  
 KW Refsum's disease; Abetalipoproteinemia; Tangier disease;

KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;  
 KW Dejerine-Sottas syndrome; Chromosome mapping; gene mapping; gene therapy;  
 KW gene; ss.  
 OS Homo sapiens.  
 XX  
 PN US2003050240-A1.  
 PD 13-MAR-2003.  
 XX  
 PF 16-OCT-2001; 2001US-00978403.  
 XX  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 03-NOV-1997; 97US-0064249P.  
 PR 13-NOV-1997; 97US-0065311P.  
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XX DT 27-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane polypeptide cDNA #36.
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XX tumour growth; retinal disorder; injury; sight loss;
XX retinitis pigmentosa; age-related macular degeneration;
XX sport-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
XX kidney disorder; mesangial cell function; Berger disease; nephropathy;
XX celiac disease; dermatitis; Crohn disease; neuropathy;
XX cardiac insufficiency disorder; peripheral neuropathy;
XX diabetic peripheral neuropathy; autonomic neuropathy;
XX atony of the urinary bladder; post polio syndrome; Krabbe's disease;
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PR 16-DEC-1999; 99US-00530095.  
PR 16-DEC-1999; 99US-00531243.  
PR 30-DEC-1999; 99US-00531274.  
PR 05-JAN-2000; 2000US-0000219.  
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PR 24-FEB-2000; 2000US-0005004.  
PR 02-MAR-2000; 2000US-0005841.  
PR 10-MAR-2000; 2000US-0006319.  
PR 21-MAR-2000; 2000US-0007532.  
PR 30-MAR-2000; 2000US-0008439.  
PR 17-MAY-2000; 2000US-0013705.













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Page 2

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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
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RESULT 3  
US-09-978-192A-161  
Sequence 161, Application US/09978192A  
Patent No. US2002017753A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
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APPLICANT: Ferrara, Napoleon  
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APPLICANT: Fong, Sherman  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
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QY	1201	CCACTGCTGTATGATCTGGGGGCGACCAACCCTGTCCGAGGAGCTCTGGGCTGCTCCG	1266
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 : GENERAL INFORMATION:  
 : APPLICANT: Ashkenazi, Avi  
 : APPLICANT: Baker Kevin P.  
 : APPLICANT: Bockstein, David  
 : APPLICANT: Deenoyers, Luc  
 : APPLICANT: Eaton, Dan  
 : APPLICANT: Ferrara, Napoleon  
 : APPLICANT: Filvaroff, Ellen  
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 : APPLICANT: Shelton, David L.  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tunas, Daniel  
 : APPLICANT: Williams, P. Mickey

1 APPLICANT: Wood, William I.  
2 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
3 ACIDS  
4 TITLE OF INVENTION: Acids Encoding the Same  
5 FILE REFERENCE: P2630P1C7  
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143 PRIOR APPLICATION NUMBER: 60/081049











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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/578,564A  
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Db	61	GGGCTTACCGCGCGGCGCAAGCGGGCGGCTCTTCGACTGCGGAGCGCTTGACGACGC	120				
QY	121	CGGAGGTGGTGGCGGGCGCGCGTGTGGTCTTGCGCTTGCGCTGATCGTGTCTCGTAGTCT	180				
Db	121	CGGAGGTGGTGGCGGGCGCGCGTGTGGTCTTGCGCTTGCGCTGATCGTGTCTCGTAGTCT	180				
QY	181	ATGGTAGGAGCTACAGCATGATGCCACAAGATCTAAGACAGATGTACTGGATTCAACCGCA	240				
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Dp	841	TGACAC	CAGTAA	GGAGCCTCA	TAGCTGG	GGGGG	CTGG	CAGAG	CAACCC	900
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Dp	1321	GGGAA	GGGCTT	TGCTTA	CAACA	CCCA	GCTTAT	TGTAA	TATTT	1380
QY	1381	GAA	GCTTGGG	AGGAG	CGGGG	TG	CCCAT	TGGCT	CCCA	1440
Dp	1381	GAA	GCTTGGG	AGGAG	CGGGG	TG	CCCAT	TGGCT	CCCA	1440
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; Publication No. US20030054405s1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David



Fri Apr 9 09:23:59 2004

us-10-020-445a-161.inpb

Page 21

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APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gettsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
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APPLICANT: Williams, P. Mickey  
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Db	1	CGACCCGCTGGGCGGACGCGTGTGGGCGGCGGAGCGGCGGACGCGGACATGAGAGCG	60			
QY	61	GGGCGCTACGGCGCGGCGCAAGGCGGGCGGCTCTTGACCTGCGGCGCTTCTGACGACG	120			
Db	61	GGGCGCTACGGCGCGGCGCAAGGCGGGCGGCTCTTGACCTGCGGCGCTTCTGACGACG	120			
QY	121	CGAGGTGGTGGCGCGCGCGCGTGTGCTTGCTTGCTTGATGCTGTTCTCTGCAATCT	180			
Db	121	CGAGGTGGTGGCGCGCGCGCGTGTGCTTGCTTGCTTGATGCTGTTCTCTGCAATCT	180			
QY	181	ATGGTAGGGCTACAGCAATGCCCAAGGTCCTAAGACAGATGATGCTGTTCAACCGCA	240			
Db	181	ATGATGAGGGCTACAGCAATGCCCAAGGTCCTAAGACAGATGATGCTGTTCAACCGCA	240			
QY	241	ACGAGAGATGCTCCGCTATGCGCATGCGCATGCGGGGTGCTGGCTTCTCTGGCTCGGCTT	300			
Db	241	ACGAGAGATGCTCCGCTATGCGCATGCGCATGCGGGGTGCTGGCTTCTCTGGCTCGGCTT	300			

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Db	301	TCCTTCGTGGTGTGACGACGATATTTCCCGACGATCAGCAACGGCACCTGACCGCAAGTACC	360
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Db	781	TTCCCATCAAGCTCTGTGAACTGTGCAGGCCCTCTCTTCAACGTGTTCAATCGTGTGAGC	840
QY	841	TGACACACAGCTTAAAGAGGCTCTATAGCTGTGGGGGGCTGGCAGAGCAACCCCAAGTG	900
Db	841	TGACACACAGCTTAAAGAGGCTCTATAGCTGTGGGGGGCTGGCAGAGCAACCCCAAGTG	900
QY	901	CCTGTGCCAGAGGGCTTCAATGACAGCCGCTCACTCTCTCCAGGGCACTTTTAAAGAAAGGT	960
Db	901	CCTGTGCCAGAGGGCTTCAATGACAGCCGCTCACTCTCTCCAGGGCACTTTTAAAGAAAGGT	960
QY	961	TTTTAGCTATGTTTTTTCCTCGCTTTTAAAGACTCAAGCCCCGCTGCAATGAGTAAAG	1020
Db	961	TTTTAGCTATGTTTTTTCCTCGCTTTTAAAGACTCAAGCCCCGCTGCAATGAGTAAAG	1020
QY	1021	CCAGCAGGTGCCATGTGCTACTGACAAAGTGCTTCAAGCTTCCCCCGGCTCGAGTCAAGC	1080
Db	1021	CCAGCAGGTGCCATGTGCTACTGACAAAGTGCTTCAAGCTTCCCCCGGCTCGAGTCAAGC	1080
QY	1081	CGTGGGAGCCGCTATTTCTGCGGTTCTCTGCAAAAGCTGTGGGGGCAATCAACCTGAC	1140
Db	1081	CGTGGGAGCCGCTATTTCTGCGGTTCTCTGCAAAAGCTGTGGGGGCAATCAACCTGAC	1140
QY	1141	CTGTGTAGCGGAGCCGAGCAAGGCTTTGTGTCTCACTCAAGTTTGTCTTCCCTGTGC	1200
Db	1141	CTGTGTAGCGGAGCCGAGCAAGGCTTTGTGTCTCACTCAAGTTTGTCTTCCCTGTGC	1200
QY	1201	CCAATGCTGATATCTGAGGGGGCAACCAACCTGTGCGGGTGTGCTCTGTGGCTGTCCG	1260
Db	1201	CCAATGCTGATATCTGAGGGGGCAACCAACCTGTGCGGGTGTGCTCTGTGGCTGTCCG	1260
QY	1261	TGTGTGTAGGGCGGGGCTGTGTCTATGTGCACTTCTCTTGTCTCCACCCCTGTGGACA	1320
Db	1261	TGTGTGTAGGGCGGGGCTGTGTCTATGTGCACTTCTCTTGTCTCCACCCCTGTGGACA	1320
QY	1321	GGGAAAGGCTTTTGCTCAACAACCCAGCTTTTATGTAATATCTGCAGTTGTATCTTAG	1380
Db	1321	GGGAAAGGCTTTTGCTCAACAACCCAGCTTTTATGTAATATCTGCAGTTGTATCTTAG	1380
QY	1381	GAAAGCTGGGGAGGGAGGGGTGCCCATGTGCTTCCAGACTCTGTCTGTGCCAGGTAT	1440

Db 1381 GAAGCTGGGAGGCGAGGGGCTCCAGCTTGTCTGTGGCGATGTAT 1440  
Qy 1441 TATTAATGTGGGAGAGATGCCCGCTGGATCTGTTGGAGACGAATTAATGTTT 1500  
Db 1441 TATTAATGTGGGAGAGATGCCCGCTGGATCTGTTGGAGACGAATTAATGTTT 1500  
Qy 1501 TGTCTTCAAG 1512  
Db 1501 TGTCTTCAAG 1512

RESULT 12  
US-09-981-915A-161  
Sequence 161, Application US/09981915A  
Publication No. US20030054986A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavira, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085697

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Matches 1512;	Conservative 0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	1	CGAGACGGTGGGCGGAGACGGCTGGGGCGGCGGAGCGGCGGCGAGCGGCGACATGGAGAGCG	60
Db	1	CGGACGGCTGGGCGGAGACGGCTGGGGCGGCGGAGCGGCGGCGAGCGGCGACATGGAGAGCG	60
QY	61	GGGCGCTACGGCGCGGCGGCGGAGCGGCGGCGCTTCGACCTTCGGCGCTTCCTGACCTAGC	120
Db	61	GGGCGCTACGGCGCGGCGGCGGAGCGGCGGCGCTTCGACCTTCGGCGCGCTTCCTGACCTAGC	120
QY	121	CGCAGAGTGTGGCGCGCGCGGTGTGGCTTCTTCGGCTTCGATCGTGTCTCCGCACTCT	180
Db	121	CGCAGAGTGTGTGGCGCGCGCGGTGTGGCTTCTTCGGCTTCGATCGTGTCTCCGCACTCT	180
QY	181	ATGTGTAGGGCTTAAGCAATATGCCAGATGTCTAAGCAGATGTACTGGTGTCAACCGCA	240
Db	181	ATGTGTAGGGCTTAAGCAATATGCCAGAGCTAAGCAGATGTACTGGTGTTCACCGCA	240
QY	241	ACGAGGATGCGCTGCGGCTATGAGCAGTGCATCGGGGTGTGGCTTCCTGAGCTCGGCT	300
Db	241	ACGAGGATGCGCTGCGGCTATGAGCAGTGCATCGGGGTGTGGCTTCCTGAGCTCGGCT	300
QY	301	TCTTCTTGTGTGTGTGAAGCGCTATTTCCGCCAGATACGCAACGCGCATGACCGCAAGTAC	360
Db	301	TCTTCTTGTGTGTGTGAAGCGCTATTTCCGCCAGATACGCAACGCGCATGACCGCAAGTAC	360
QY	361	TGTCATTTGTGACCTCTCTTCTCACTCTCTGACCTTCGACCTTCCTGTGTGTGTGTCT	420
Db	361	TGTCATTTGTGACCTCTCTTCTCACTCTCTGACCTTCGACCTTCCTGTGTGTGTGTCT	420
QY	421	GCTTCTTACCAACGATGGGCGAGTCAACCCGAAAGACGTGTGTGTGGGGCGGACT	480
Db	421	GCTTCTTACCAACGATGGGCGAGTCAACCCGAAAGACGTGTGTGTGGGGCGGACT	480
QY	481	CTGTGAGGGGCGGCATCACTTCAGCTTCTTTTCATCTTCTCCTGGGGTGTGTGACT	540
Db	481	CTGTGAGGGGCGGCATCACTTCAGCTTCTTTTCATCTTCTCCTGGGGTGTGTGACT	540
QY	541	CCCTGGCGCTACGAGCGCTACAGGCTGGCGTGAACAATTCATCCAGAAATTAAGCTTAC	600
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QY	601	CCACTCCGGAACCCCAACATCTGCTACGCGCTCTTACCCAGGTGCACTGTGTGACAACTACC	660
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QY	661	AACAGCCACCTTTACACCGAAGACCGGGAAGACACCGAGGGCTAACCAACCGCCCGCTGT	720
Db	661	AACAGCCACCTTTACACCGAAGACCGGGAAGACACCGAGGGCTAACCAACCGCCCGCTGT	720
QY	721	ACTGAGTGGCGGTAGCGTGGGAAGGGGGAACAGAGAGGCGCTCCCTCTGACCTTGACT	780
Db	721	ACTGAGTGGCGGTAGCGTGGGAAGGGGGAACAGAGAGGCGCTCCCTCTGACCTTGACT	780
QY	781	TTCCCATATAGGCTCTGTGAATGCGCAACCGCTCTCTTCACTGTTCATTCCTGTGAGC	840
Db	781	TTCCCATATAGGCTCTGTGAATGCGCAACCGCTCTCTTCACTGTTCATTCCTGTGAGC	840
QY	841	TGACACACAGCTAAGAGCGCTCATATAGCTGTGGCGGGGCTGTGACAGCCACACCCCAAGTG	900
Db	841	TGACACACAGCTAAGAGCGCTCATATAGCTGTGGCGGGGCTGTGACAGCCACACCCCAAGTG	900
QY	901	CCTGTGCCCAAGGGGCTTCAGTACGCGGCTCATGCTCCACAGGGGCACTTTTAGGAAAGGT	960
Db	901	CCTGTGCCCAAGGGGCTTCAGTACGCGGCTCATGCTCCACAGGGGCACTTTTAGGAAAGGT	960
QY	961	TTTTAGCTAGTGTCTTCGCGCTTTTAATGACCTACGCCCCGCTGCAAGTGTGCTAAG	1020
Db	961	TTTTAGCTAGTGTCTTCGCGCTTTTAATGACCTACGCCCCGCTGCAAGTGTGCTAAG	1020
QY	1021	CGAGAGGTGCCCATGTGTACTACAAAGTGCCTCACTTCCCGCGGCGCGGCTCAAGG	1080
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 QY 1321 GGGAGGCGCTTGTCTGACACACCCAGCTTGTGTAAATTTCTGCACTGTTACTTG 1380  
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 QY 1501 TCTCATTCGAAG 1512  
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RESULT 13

US-09-978-824-161  
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 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi  
 / APPLICANT: Baker Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnovers, Luc  
 / APPLICANT: Eaton, Dan  
 / APPLICANT: Ferrara, Napoleon  
 / APPLICANT: Filvaroff, Ellen  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerltisen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Guiney, Austen L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Kijavini, Ivar J.  
 / APPLICANT: Kuo, Sophia S.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Shelton, David L.  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / FILE REFERENCE: P2630PIC14  
 / CURRENT APPLICATION NUMBER: US/09/978,824  
 / PRIOR FILING DATE: 2001-10-17  
 / PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085333
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US-09-978-423A-161
Sequence 161, Application US/09978423A
Publication No. US20030069178A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
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Search completed: April 8, 2004, 10:02:50  
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XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;		
XX	WPI: 1999-551358/46.		
XX	P-PSDB; ANY41709.		
XX	New secreted and transmembrane polypeptides and their polynucleotides		

PT useful for treating blood coagulation disorders, cancers and cellular  
adhesion disorders.

XX Claim 2, Fig 60, 530pp, English.

XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to  
CC AA41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention

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Best Local Similarity 100.0%; Pident. No. 0;  
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RESULT 3  
ID AAC58232 standard; cDNA; 1512 BP.  
AAC58232;  
25-JAN-2001 (first entry)  
Human PRO615 nucleotide sequence SEQ ID NO:15.  
Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
tumorigenesis; detection; neoplastic cell growth; proliferation;  
cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;  
immunological disorder; ss.  
Homo sapiens.  
WO200053754-A1.  
14-SEP-2000.  
06-JAN-2000; 2000WO-US000277.  
08-MAR-1999; 99WO-US005028.  
12-MAR-1999; 99US-0123957P.  
29-MAR-1999; 99US-0126773P.  
21-APR-1999; 99US-010232P.  
28-APR-1999; 99US-0131445P.  
05-OCT-1999; 99WO-US023089.  
30-NOV-1999; 99WO-US028313.  
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02-DEC-1999; 99WO-US031243.  
30-DEC-1999; 99WO-US031274.  
(GENTH ) GENENTECH INC.  
Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA,  
Wood WJ;  
WPI; 2000-572269/53.  
P-PSDB; AAB24048.  
New isolated antibody for use in compositions and methods for the  
diagnosis and treatment of neoplastic cell growth and proliferation in  
mammals, including humans, and in monitoring tumor treatment.  
Claim 50; Fig 15; 195pp; English.  
The present invention describes an isolated antibody (Ab) that binds to  
one of the human proteins (P) designated PRO213, PRO1330, PRO149,  
PRO337, PRO324, PRO351, PRO615, PRO538, PRO3664, PRO618,  
PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions and  
methods for the diagnosis and treatment of neoplastic cell growth and  
proliferation in mammals, including humans. Genes and polypeptides  
encoded by them, that are amplified in the genome of a tumour cell, can  
be identified and are useful targets for the treatment and prevention of  
certain cancers and may be used to monitor tumor treatment. Compounds





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PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-0004022C.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
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PR 17-MAY-2000; 98US-0033565P.  
PR 22-MAY-2000; 98US-0033565P.  
PR 30-MAY-2000; 98US-0033565P.



XX Novel human secreted and transmembrane protein PRO615 cDNA.  
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 XX Human; secreted and transmembrane protein; PRO; anti-inflammatory;  
 XX anti-atherosclerotic; cardiatic; anti-infectivity; anti-HIV; cytostatic;  
 KM anti-atherosclerotic; gene therapy; inflammatory disease; organ failure;  
 KM atherosclerosis; cardiac injury; infertility; birth defect;  
 KM premature aging; AIDS; cancer; diabetic complication; chromosome mapping;  
 KM Gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;  
 KM tissue typing; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN US2002192706-A1.  
 XX  
 PD 19-DEC-2002.  
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 PF 24-OCT-2001; 2001US-00999832.  
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 XX 17-OCT-1997; 97US-0062250P.  
 XX 03-NOV-1997; 97US-0064249P.  
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 PR 22-APR-1998; 98US-0082700P.  
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 PR 20-NOV-1998; 98WO-US024855.  
 PR 05-JAN-1999; 99WO-US000106.  
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PR 10-MAR-1999; 99WO-US005190.  
 PR 14-MAY-1999; 99WO-US010733.  
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 PR 02-DEC-1999; 99WO-US028551.  
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 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
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 PR 06-JAN-2000; 2000WO-US002777.  
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 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
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 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 26-JUN-2000; 2000WO-US020710.  
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 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Flvayroff E, Fong S, Gao W, Garber H, Gerritsen ME;  
 PI Goddard A, Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart JA, Tumas D, Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-328860/31.  
 DR P-PSDB; AB072217.  
 DR  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides, designated  
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
 PT cancer.  
 XX  
 PS Claim 2; Fig 60; 453pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid (I) comprising, or which  
 CC is at least 80 % sequence identity to, or the full-length coding sequence  
 CC of, any of 118 300-2100 nucleotide sequences, which encodes its  
 CC corresponding PRO polypeptide selected from 118 100-700 amino acid  
 CC sequences, all given in the specification. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS, cancer, or diabetic complications. The nucleic  
 CC acids are useful as hybridisation probes, in chromosome and gene mapping,  
 CC and in generating antisense RNA or DNA. The polypeptides are useful as  
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful  
 CC in tissue typing. This sequence encodes a novel human secreted and  
 CC transmembrane PRO polypeptide  
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 SQ Sequence 1512 BP; 246 A; 482 C; 446 G; 338 T; 0 U; 0 Other;

Query March 100.0%; Score 1512; DB 7; Length 1512;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 901 CCTGTGGCCAGAGGGCTTCAATCAGCGCTTCACTTCTTCAAGGGAGCTTTTAAAGAGGT 960
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QY 961 TTTTATGAGTGTTTTCTGCTTTTAAATGACTTCAAGCCCGGCTGAGTGGCTAGAG 1020
Db 961 TTTTATGAGTGTTTTCTGCTTTTAAATGACTTCAAGCCCGGCTGAGTGGCTAGAG 1020
QY 1021 CCAAGAGGTGGCCATGTGCTTCAAGAGTGGCTTCACTTCCCGGCGGCGGCTGAGG 1080
Db 1021 CCAAGAGGTGGCCATGTGCTTCAAGAGTGGCTTCACTTCCCGGCGGCGGCTGAGG 1080
QY 1081 CGTGGAGCCCGCTATTTATCTGCTTCTGCAAAAGACTCGTGGGAGGCTACACCTGC 1140

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Db 1081 CGTGGAGCCCGCTATTTATCTGCTTCTGCAAAAGACTCGTGGGAGGCTACACCTGC 1140
QY 1141 CCTGTGACAGCGGAGCGGAGCCAGCTTGTGTCTTCTTCACTAGTGTTCCTTCCCTG 1200
Db 1141 CCTGTGACAGCGGAGCGGAGCCAGCTTGTGTCTTCTTCACTAGTGTTCCTTCCCTG 1200
QY 1201 CCACTGTGTATGATCTGGGAGGACACACCCCTGTGCGGAGCTTGGCTTGGCTTGG 1260
Db 1201 CCACTGTGTATGATCTGGGAGGACACACCCCTGTGCGGAGCTTGGCTTGGCTTGG 1260
QY 1261 TGGTGTGAGGGCGGAGGCTGTGTCTTATGAGCACTTCTTCTTCTTCTTCTTCTT 1320
Db 1261 TGGTGTGAGGGCGGAGGCTGTGTCTTATGAGCACTTCTTCTTCTTCTTCTTCTT 1320
QY 1321 GGGAGAGGCTTGGCTTGGCAACACCCAGCTTATGATTAATTTGCAAGTGTACTAG 1380
Db 1321 GGGAGAGGCTTGGCTTGGCAACACCCAGCTTATGATTAATTTGCAAGTGTACTAG 1380
QY 1381 GAAGCCTGGGAGGAGGAGGCTGCCCATGCTCCAGACTCTGTCTGTGCCAGTGTAT 1440
Db 1381 GAAGCCTGGGAGGAGGAGGCTGCCCATGCTCCAGACTCTGTCTGTGCCAGTGTAT 1440
QY 1441 TATTAATCTGTGGGAGGAGTGGCCGCGGAGTGGTGGTGGAGAGCGGAATTAATGTT 1500
Db 1441 TATTAATCTGTGGGAGGAGTGGCCGCGGAGTGGTGGTGGAGAGCGGAATTAATGTT 1500
QY 1501 TCTCATTCMAAG 1512
Db 1501 TCTCATTCMAAG 1512

RESULT 6
ACAT1759
ID ACAT1759 standard; cDNA; 1512 BP.
XX
AC ACAT1759;
DT 11-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane polypeptide PRO615 cDNA.
XX
KW Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 21-NOV-1997; 97US-0065311P.
PR 11-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.

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QY	361	TGATATATGATACCTGCTCTTCTCAAGCTCTTGAGACTTCTCTGTGGTTTGTGGTTCT	420
Db	361	TGGTATATGGTAACTGCTCTTCTCAAGCTCTTGAGACTTCTCTGTGGTTTGTGGTTCT	420
QY	421	GCTTCTCAACCAAGTGGGAGTCAACCAACCGAAGACGTGTGGTGGGGCCGACT	480
Db	421	GCTTCTCAACCAAGTGGGAGTCAACCAACCGAAGACGTGTGGTGGGGCCGACT	480
QY	481	CTGTAGGGGACCAATACCTTCAAGTTCTTTCATCTTCTCCGAGGTGTGTGGCT	540
Db	481	CTGTAGGGGACCAATACCTTCAAGTTCTTTCATCTTCTCCGAGGTGTGTGGCT	540
QY	541	CCCTGGCTTACCAAGGCTTCAAGGCTGGGTGAGACTTTCATCCAGATTACTGTGACC	600
Db	541	CCCTGGCTTACCAAGGCTTCAAGGCTGGGTGAGACTTTCATCCAGATTACTGTGACC	600
QY	601	CCACTCCGGACCCCAACTGTGCTTACGCTTCAACCAAGTGCATCTGTGACAATCAC	660
Db	601	CCACTCCGGACCCCAACTGTGCTTACGCTTCAACCAAGTGCATCTGTGACAATCAC	660
QY	661	AACAGCAACCTTCAACCGAGAACCGGAGACCAAGGAGCTTCAACGACCGCCCTGTGT	720
Db	661	AACAGCAACCTTCAACCGAGAACCGGAGACCAAGGAGCTTCAACGACCGCCCTGTGT	720
QY	721	ACTGATGGCGGTTTGGCGTGGGAGAGGGGGACAGAGGGGCGTCCCTGCTGGCTGACT	780
Db	721	ACTGATGGCGGTTTGGCGTGGGAGAGGGGGACAGAGGGGCGTCCCTGCTGGCTGACT	780
QY	781	TTCCCATGAGCTCTGTGAACCTGCCAGCGCCCTCTCTTTCACCTGTTCATCCTGTGACG	840
Db	781	TTCCCATGAGCTCTGTGAACCTGCCAGCGCCCTCTCTTTCACCTGTTCATCCTGTGACG	840
QY	841	TGACACACAGCTCAAGAGAGGCTCATAGGCTGGGGGGCTGGAGAGCCACACCCCAATG	900
Db	841	TGACACACAGCTCAAGAGAGGCTCATAGGCTGGGGGGCTGGAGAGCCACACCCCAATG	900
QY	901	CCTGTGCCCAAGGGCTTTCAGTCAAGCGGCTCATCTTCCAGGGACACTTTTAGAAAGGT	960
Db	901	CCTGTGCCCAAGGGCTTTCAGTCAAGCGGCTCATCTTCCAGGGACACTTTTAGAAAGGT	960
QY	961	TTTTAGCTAGTATTTTTTCTGCTTTTATATGACTCAGCGCCGCTCGAGAGGACTAGAG	1020
Db	961	TTTTAGCTAGTATTTTTTCTGCTTTTATATGACTCAGCGCCGCTCGAGAGGACTAGAG	1020
QY	1021	CCAGCAGGTGCCATGTGCTACTGACAAAGTGCCTAGCTTCCGCCGAGCTCAAGC	1080
Db	1021	CCAGCAGGTGCCATGTGCTACTGACAAAGTGCCTAGCTTCCGCCGAGCTCAAGC	1080
QY	1081	CGTGGAGACCGCTTATATCTGTGCTCTGTGCACAAAGACTCGTGGGGGGCATATCACCTG	1140
Db	1081	CGTGGAGACCGCTTATATCTGTGCTCTGTGCACAAAGACTCGTGGGGGGCATATCACCTG	1140
QY	1141	CCTGTGCAGCGGACCGGACCAAGGCTCTTGTGTCTTCACTCAGGTTTCTTCCCTGTGC	1200
Db	1141	CCTGTGCAGCGGACCGGACCAAGGCTCTTGTGTCTTCACTCAGGTTTCTTCCCTGTGC	1200
QY	1201	CCACTGCTGTATGATCTGGGGGGCACCAACCTGTGCAGGTGGCTCTGAGGCTGCTCCG	1260
Db	1201	CCACTGCTGTATGATCTGGGGGGCACCAACCTGTGCAGGTGGCTCTGAGGCTGCTCCG	1260
QY	1261	TGGTGTAGAGGCTGGGCTGTGTCTCATGGCACTTCTCTTGTCTCCACCCCTGGAGCA	1320
Db	1261	TGGTGTAGAGGCTGGGCTGTGTCTCATGGCACTTCTCTTGTCTCCACCCCTGGAGCA	1320
QY	1321	GAGAAAGGACTTGTCTGTACAAACACCAAGCTTATATTAATTTGTGCAAGTTGTACTAG	1380
Db	1321	GAGAAAGGACTTGTCTGTACAAACACCAAGCTTATATTAATTTGTGCAAGTTGTACTAG	1380
QY	1381	GAAAGCTTGGAGAGGACAGGGGTGCCCATAGTCTCCAGACTCTGTCTGTGCCAGATGTAT	1440
Db	1381	GAAAGCTTGGAGAGGACAGGGGTGCCCATAGTCTCCAGACTCTGTCTGTGCCAGATGTAT	1440

QY	1441	TATAAATCGGGGGAGATGCCCGGCTGGGAATGCTTTGGGAGACGGAATTAATGTTT	1500
Db	1441	TATATAATCGGTGGGGAGATGCCCGGCTGGGAATGCTTTGGAGACGGAATTAATGTTT	1500
QY	1501	TCTCATTCAAG 1512	
Db	1501	TCTCATTCAAG 1512	
RESULT 7			
ABX92399			
ID	ABX92399	standard; cDNA, 1512 BP.	
XX			
AC	ABX92399;		
DT			
XX	08-MAY-2003	(first entry)	
DE			
XX		cDNA encoding human PRO615 polypeptide.	
KW		Human; PRO polypeptide; secreted and transmembrane protein;	
KW		immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;	
KW		cardiac insufficiency; nervous system disorder; kidney disorder;	
KW		bone disorder; cartilage disorder; arthritis; tumour; wound healing;	
KW		genetic disorder; cytostatic; antidiabetic; antiinflammatory;	
KW		antiarthritic; anti-tumour; vulnery; antiansemic; dermatological;	
KW		cardiant; gene; ss.	
XX			
OS		Homo sapiens.	
XX			
XX		US2002169284-A1.	
XX			
PD	14-NOV-2002.		
XX			
PF	16-OCT-2001; 2001US-00978697.		
XX			
PR	26-MAY-1981;	81US-00267213.	
PR	17-OCT-1987;	97US-0062250P.	
PR	03-NOV-1997;	97US-0064249P.	
PR	13-NOV-1997;	97US-0065311P.	
PR	21-NOV-1997;	97US-0066364P.	
PR	10-MAR-1998;	98US-0077450P.	
PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-00776641P.	
PR	11-MAR-1998;	98US-0077664P.	
PR	12-MAR-1998;	98US-0077791P.	
PR	13-MAR-1998;	98US-0078004P.	
PR	17-MAR-1998;	98US-00040220.	
PR	20-MAR-1998;	98US-0078886P.	
PR	20-MAR-1998;	98US-0078910P.	
PR	20-MAR-1998;	98US-0078936P.	
PR	20-MAR-1998;	98US-0078939P.	
PR	25-MAR-1998;	98US-0079294P.	
PR	26-MAR-1998;	98US-0079655P.	
PR	27-MAR-1998;	98US-0079663P.	
PR	27-MAR-1998;	98US-0079664P.	
PR	27-MAR-1998;	98US-0079689P.	
PR	27-MAR-1998;	98US-0079728P.	
PR	27-MAR-1998;	98US-0079786P.	
PR	30-MAR-1998;	98US-0079920P.	
PR	30-MAR-1998;	98US-0079923P.	
PR	26-JUN-1998;	98US-00105413.	
PR	07-OCT-1998;	98US-00168978.	
PR	07-OCT-1998;	98WO-US021141.	
PR	02-NOV-1998;	98US-00184216.	
PR	06-NOV-1998;	98US-00187368.	
PR	20-NOV-1998;	98WO-US024855.	
PR	07-DEC-1998;	98US-00202054.	
PR	22-DEC-1998;	98US-00218517.	
PR	05-JAN-1999;	99WO-US000106.	
PR	05-MAR-1999;	99US-00254465.	
PR	08-MAR-1999;	99WO-US005028.	
PR	10-MAR-1999;	99US-00265686.	
PR	10-MAR-1999;	99WO-US005190.	

PR 12-APR-1999; 99US-00284291.  
 PR 14-MAY-1999; 99US-0031832.  
 PR 14-MAY-1999; 99MO-US010733.  
 PR 02-JUN-1999; 99MO-US012252.  
 PR 25-AUG-1999; 99US-00380137.  
 PR 25-AUG-1999; 99US-00380138.  
 PR 25-AUG-1999; 99US-00380142.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 02-DEC-1999; 99MO-US028551.  
 PR 02-DEC-1999; 99MO-US030095.  
 PR 30-DEC-1999; 99MO-US031243.  
 PR 30-DEC-1999; 99MO-US031274.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000277.  
 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004341.  
 PR 24-FEB-2000; 2000MO-US005004.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 10-MAR-2000; 2000MO-US006319.  
 PR 21-MAR-2000; 2000MO-US007532.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 27-NOV-2000; 2000US-00723749.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000MO-US034956.  
 PR 28-FEB-2001; 2001MO-US006520.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 22-MAR-2001; 2001US-00816920.  
 PR 22-MAR-2001; 2001MO-US009552.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 10-MAY-2001; 2001MO-US017092.  
 PR 25-MAY-2001; 2001MO-US017035.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 05-JUN-2001; 2001MO-US017800.  
 PR 14-JUN-2001; 2001US-00874503.  
 PR 19-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001MO-US019592.  
 PR 29-JUN-2001; 2001MO-US021066.  
 PR 09-JUL-2001; 2001MO-US021735.  
 PR 30-JUL-2001; 2001US-00918585.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;  
 PI Ferrara N, Fliszaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;  
 PI Goodfellow A, Godowski PJ, Grimaldi JC, Gurney KM, Hillan KJ;  
 PI Kijavich IJ, Kuo SS, Napier MA, Pan J, Paoletti NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tamas D, Williams FM, Wood WI;  
 XX  
 DR WPI: 2003-288163/28.  
 DR P-PSDB; AB061095.  
 XX  
 PT Novel secreted and transmembrane polypeptides and polynucleotides  
 PT encoding them useful for treating cancer, kidney diseases, bone,  
 PT cartilage disorders and immune deficiencies.  
 XX  
 PS Claim 2; Fig 60; 459pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating

CC biological activities of cells expressing PRO polypeptides, and for for  
 CC identifying agonists or antagonists. The bioactive molecule maybe a  
 CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.  
 CC The PRO polypeptides are useful for treating immune disorders, diabetes  
 CC or hyper- or hypo-insulinemia, cardiac insufficiency, nervous system  
 CC disorders, kidney disorders, bone and cartilage disorders or arthritis,  
 CC tumours, and wound healing. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and gene  
 CC mapping, in the generation of antisense RNA and DNA, in the preparation  
 CC of PRO polypeptides, for generating transgenic animals or knockout  
 CC animals, for the genetic analysis of individuals with genetic disorders,  
 CC and in gene therapy. The present sequence encodes a human PRO polypeptide  
 CC of the invention. Note: The sequence data for this patent was obtained in  
 CC electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdidentry.html  
 XX  
 SQ Sequence 1512 BP; 246 A; 482 C; 446 G; 338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1512; DB 7; Length 1512;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACGGGTGGGCGGAGCGGCTGGGCGGCGGCGGAGCGGCGGAGCATGAGAGCG 60  
 DB 1 CGGACGGGTGGGCGGAGCGGCTGGGCGGCGGCGGAGCGGCGGAGCATGAGAGCG 60  
 QY 61 GGGCTTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 DB 61 GGGCTTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 QY 121 CGGAGGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 DB 121 CGGAGGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 QY 181 ATGCTGAGGCTTACGAGATGCCAGAGTCTTACGAGATGCTGCTTACGAGCA 240  
 DB 181 ATGCTGAGGCTTACGAGATGCCAGAGTCTTACGAGATGCTGCTTACGAGCA 240  
 QY 241 ACGAGAGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 DB 241 ACGAGAGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 QY 301 TCTTCTTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 DB 301 TCTTCTTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 QY 361 TGGTCATTTGGAGACCTGCTCTTCAAGTCTTCTTCAAGTCTTCTTCAAGTCTTCTTCAAG 420  
 DB 361 TGGTCATTTGGAGACCTGCTCTTCAAGTCTTCTTCAAGTCTTCTTCAAGTCTTCTTCAAG 420  
 QY 421 GCTTCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 480  
 DB 421 GCTTCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 480  
 QY 481 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 DB 481 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 QY 541 CCTGGGCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600  
 DB 541 CCTGGGCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600  
 QY 601 CCACTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 DB 601 CCACTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 QY 661 AACAGCCACCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCA 720  
 DB 661 AACAGCCACCTTACCAACCAAGTGGGAGTCAACCAACCAACCAACCAACCAACCAACCAACCA 720  
 QY 721 ACTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 DB 721 ACTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

QY 781 TTCCATGAGCCTCTGGAACTGCGAGGCCCTCTTCACTGTTCCATCTGTGAGC 840  
DB 781 TTCCATGAGCCTCTGGAACTGCGAGGCCCTCTTCACTGTTCCATCTGTGAGC 840  
QY 841 TGACACAGAGCTTAAGAGAGCTTATAGCCTGGCGGGGCTGGCAGAGCCACCCCAAGT 900  
DB 841 TGACACAGAGCTTAAGAGAGCTTATAGCCTGGCGGGGCTGGCAGAGCCACCCCAAGT 900  
QY 901 CCTGGGCCAGAGGCTTACAGTACAGCCGCTCACTCTTCCAGGACCTTTTGGAAAGGT 960  
DB 901 CCTGGGCCAGAGGCTTACAGTACAGCCGCTCACTCTTCCAGGACCTTTTGGAAAGGT 960  
QY 961 TTTAGTAGTATTTTCTCTGCTTTTATGACCTCAGCCCGGCTGAGTGGCTAGAG 1020  
DB 961 TTTAGTAGTATTTTCTCTGCTTTTATGACCTCAGCCCGGCTGAGTGGCTAGAG 1020  
QY 1021 CCAGCAGGTGCCCATGTGCTACTGACAAAGTGCCTCAGCTTCCCGGCGGCTCAGGC 1080  
DB 1021 CCAGCAGGTGCCCATGTGCTACTGACAAAGTGCCTCAGCTTCCCGGCGGCTCAGGC 1080  
QY 1081 CGTGGAGCGGCTATTTATCTGCTGCTGCGCAAGATCGGAGGGGACATCAGACCTGC 1140  
DB 1081 CGTGGAGCGGCTATTTATCTGCTGCTGCGCAAGATCGGAGGGGACATCAGACCTGC 1140  
QY 1141 CCTGTGACAGCGAGCGGACAGGCTTGTGTCTCACTCAGGTTGCTTCCCTGTGC 1200  
DB 1141 CCTGTGACAGCGAGCGGACAGGCTTGTGTCTCACTCAGGTTGCTTCCCTGTGC 1200  
QY 1201 CCACGCTGTATGATCTGGGGGCGCACCACTGTGCGGGTGGCTGGCTGCCG 1260  
DB 1201 CCACGCTGTATGATCTGGGGGCGCACCACTGTGCGGGTGGCTGGCTGCCG 1260  
QY 1261 TGTGTGAGGGGCGGCTGTGCTCATGCACTTCTCTTGTCCACCCCTG3CAGCA 1320  
DB 1261 TGTGTGAGGGGCGGCTGTGCTCATGCACTTCTCTTGTCCACCCCTG3CAGCA 1320  
QY 1321 GGGAGGGCTTTGCTGACAAACCCAGCTTTATGTAATTTGCGAGTGTACTTAG 1380  
DB 1321 GGGAGGGCTTTGCTGACAAACCCAGCTTTATGTAATTTGCGAGTGTACTTAG 1380  
QY 1381 GAAGCCTGGGAGGCGCAGGGGTGCCCATGCTGCCAGCTGTGTGCGAGTAT 1440  
DB 1381 GAAGCCTGGGAGGCGCAGGGGTGCCCATGCTGCCAGCTGTGTGCGAGTAT 1440  
QY 1441 TATTAATCTGTGGGAGATGCCGCGCTGGATGCTTTGGAGACGGAATTAATGTTT 1500  
DB 1441 TATTAATCTGTGGGAGATGCCGCGCTGGATGCTTTGGAGACGGAATTAATGTTT 1500  
QY 1501 TCTCATTCAGAG 1512  
DB 1501 TCTCATTCAGAG 1512

RESULT 8  
ACA66140  
ID ACA66140 standard; cDNA; 1512 BP.  
XX ACA66140;  
XX 24-JUN-2003 (first entry)  
XX Human cDNA encoding secreted/transmembrane protein PRO615.  
XX  
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;  
XX malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;  
XX leukemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;  
XX infertility; premature aging; psoriasis; inflammatory disease;  
XX renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;  
XX hepatitis; multiple sclerosis; gene therapy.  
OS Homo sapiens.  
XX

PN US2003004102-A1.  
XX 02-JAN-2003.  
XX  
XX 15-OCT-2001; 2001US-00978189.  
XX  
XX 17-OCT-1997; 97US-0062250P.  
XX 03-NOV-1997; 97US-0064249P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 21-NOV-1997; 97US-0066364P.  
XX 11-MAR-1998; 98US-0077450P.  
XX 11-MAR-1998; 98US-0077632P.  
XX 11-MAR-1998; 98US-0077641P.  
XX 11-MAR-1998; 98US-0077649P.  
XX 12-MAR-1998; 98US-0077751P.  
XX 13-MAR-1998; 98US-0078004P.  
XX 17-MAR-1998; 98US-00840220.  
XX 20-MAR-1998; 98US-0078886P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 20-MAR-1998; 98US-0078936P.  
XX 20-MAR-1998; 98US-0078939P.  
XX 25-MAR-1998; 98US-0079294P.  
XX 25-MAR-1998; 98US-0079656P.  
XX 27-MAR-1998; 98US-0079663P.  
XX 27-MAR-1998; 98US-0079664P.  
XX 27-MAR-1998; 98US-0079689P.  
XX 27-MAR-1998; 98US-0079728P.  
XX 27-MAR-1998; 98US-0079786P.  
XX 30-MAR-1998; 98US-0079920P.  
XX 30-MAR-1998; 98US-0079923P.  
XX 25-JUN-1998; 98US-00105413.  
XX 07-OCT-1998; 98US-00168978.  
XX 07-OCT-1998; 98US-00211141.  
XX 02-NOV-1998; 98US-00184216.  
XX 06-NOV-1998; 98US-00187368.  
XX 20-NOV-1998; 98US-0024855.  
XX 07-DEC-1998; 98US-00202054.  
XX 22-DEC-1998; 98US-00218517.  
XX 05-JAN-1999; 99US-0000106.  
XX 05-MAR-1999; 99US-00254465.  
XX 08-MAR-1999; 99US-00250528.  
XX 10-MAR-1999; 99US-00265686.  
XX 10-MAR-1999; 99US-00265190.  
XX 12-MAR-1999; 99US-00267213.  
XX 12-APR-1999; 99US-00284291.  
XX 14-MAY-1999; 99US-00311832.  
XX 02-JUN-1999; 99US-00312252.  
XX 25-AUG-1999; 99US-00380137.  
XX 25-AUG-1999; 99US-00380138.  
XX 25-AUG-1999; 99US-00380142.  
XX 30-NOV-1999; 99US-00382313.  
XX 02-DEC-1999; 99US-00382851.  
XX 02-DEC-1999; 99US-00382855.  
XX 16-DEC-1999; 99US-00390095.  
XX 30-DEC-1999; 99US-00391243.  
XX 30-DEC-1999; 99US-00391274.  
XX 05-JAN-2000; 2000US-0000219.  
XX 06-JAN-2000; 2000US-0000277.  
XX 11-FEB-2000; 2000US-0000376.  
XX 18-FEB-2000; 2000US-0000385.  
XX 24-FEB-2000; 2000US-0000341.  
XX 01-MAR-2000; 2000US-0000504.  
XX 01-MAR-2000; 2000US-0005601.  
XX 10-MAR-2000; 2000US-0005841.  
XX 10-MAR-2000; 2000US-0006319.  
XX 21-MAR-2000; 2000US-0006732.  
XX 30-MAR-2000; 2000US-0006435.  
XX 17-MAY-2000; 2000US-0013705.  
XX 22-MAY-2000; 2000US-0014042.  
XX 30-MAY-2000; 2000US-0014941.  
XX 02-JUN-2000; 2000US-0015264.  
XX 28-JUL-2000; 2000US-0020710.



PR	24-AUG-2000	2000MO-US023328
PR	08-NOV-2000	2000MO-US079928
PR	27-NOV-2000	2000MO-US030873
PR	12-NOV-2000	2000MO-US072749
PR	01-DEC-2000	2000MO-US036748
PR	20-DEC-2000	2000MO-US074752
PR	20-DEC-2000	2000MO-US034956
PR	28-FEB-2001	2001MO-US006520
PR	28-MAR-2001	2001MO-US081644
PR	22-MAR-2001	2001MO-US081620
PR	22-MAR-2001	2001MO-US093552
PR	10-MAY-2001	2001US-00854208
PR	25-MAY-2001	2001US-00854280
PR	01-JUN-2001	2001MO-US051792
PR	01-JUN-2001	2001US-00872035
PR	05-JUN-2001	2001MO-US0517800
PR	14-JUN-2001	2001US-00874503
PR	19-JUN-2001	2001US-00882636
PR	19-JUN-2001	2001MO-US086542
PR	29-JUL-2001	2001MO-US021066
PR	30-JUL-2001	2001MO-US021755
PR	30-JUL-2001	2001US-00918585

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Boesteln D, Denoyers J, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gershen ME, Goddard A, Grimaldi JC, Gurney AL, Hillan KJ, Kluvian TJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL, Stewart TA, Williams PM, Wood WJ, Tumas D

PT New genes and secreted and transmembrane polypeptides (e.g. PR0337 or PT PR0159), useful for treating or diagnosing e.g. cancers, PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 2; Fig 60; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or (c) the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, perioritis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

Db 961 TTTAGCTAGTGTTCCTCGCTTTATAGACCTGACCCCGCTCAGTGGCTAGAAG 1020  
QY 1021 CCAGACAGTGGCCCTGCTGCTACTACACAAGTGCCTCAGCTTCCCCCGCCGCTCAGGC 1080  
Db 1021 CCAGACAGTGGCCCTGCTGCTACTACACAAGTGCCTCAGCTTCCCCCGCCGCTCAGGC 1080  
QY 1081 CGTGGAGCCGCTATTATCTGCGTCTCTGCTCCAAAGACTGCTGGGGGCATCACACCTGC 1140  
Db 1081 CGTGGAGCCGCTATTATCTGCGTCTCTGCTCCAAAGACTGCTGGGGGCATCACACCTGC 1140  
QY 1141 CTTGTGACGCGGACCGGACCGAGCTCTGTGCTCTCCTAGTGGTTGCTTCCCTGTGC 1200  
Db 1141 CTTGTGACGCGGACCGGACCGAGCTCTGTGCTCTCCTAGTGGTTGCTTCCCTGTGC 1200  
QY 1201 CCAGCTGCTGATGATCTGCGGGGACCAACCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1260  
Db 1201 CCAGCTGCTGATGATCTGCGGGGACCAACCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1260  
QY 1261 TGGTGTGAGGGCGGGGCTGCTGCTCATGAGCACTTCTCTCTTCTCCACCCCTGGAGCA 1320  
Db 1261 TGGTGTGAGGGCGGGGCTGCTGCTCATGAGCACTTCTCTCTTCTCCACCCCTGGAGCA 1320  
QY 1321 GGGAGGCGCTTGGCTGACACACCGAGCTTATGTAATTTCTGCACTTGTACTTGG 1380  
Db 1321 GGGAGGCGCTTGGCTGACACACCGAGCTTATGTAATTTCTGCACTTGTACTTGG 1380  
QY 1381 GAAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440  
Db 1381 GAAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440  
QY 1441 TATATAATCGTGGGAGAGATCCCGGCTGGAGAGCTGCTTGGAGAGGAGTAATGTTT 1500  
Db 1441 TATATAATCGTGGGAGAGATCCCGGCTGGAGAGCTGCTTGGAGAGGAGTAATGTTT 1500  
QY 1501 TCTCATTCGAAG 1512  
Db 1501 TCTCATTCGAAG 1512

RESULT 9  
ADA24700  
ID ADA24700 standard; cDNA; 1512 BP.  
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AC ADA24700;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO615 cDNA.  
XX  
KW Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;  
KW chromosome identification; vaccine; cancer; retinal disorder;  
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;  
KW wound healing; obesity; diabetes; hearing loss;  
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;  
KW haemoglobin associated disorder.  
XX  
OS Homo sapiens.  
XX  
PN US2003050241-A1.  
XX  
FD 13-MAR-2003.  
XX  
PF 16-OCT-2001; 2001US-00978564.  
XX  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
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PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
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PR 01-APR-1998; 98US-0080332P.  
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PR 07-MAY-1998; 98US-0084637P.  
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PR 07-MAY-1998; 98US-0084640P.  
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PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.



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Db 721 ACTGATGAGGCGGTGATGCGTGGAGAGGGGAGAGAGGCGCCCTGCTCCCTGACT 780
QY 781 TTCCCATAGAGCCTCTGAGAACCTGACAGCCCTCTCTTCAACCTGCTCCCTGACT 840
Db 781 TTCCCATAGAGCCTCTGAGAACCTGACAGCCCTCTCTTCAACCTGCTCCCTGACT 840
QY 841 TGAACACAGAGTAAAGAGAGCCTCATAGCCTGCGGGGGGCTGGCAAGCCACCCCAAGT 900
Db 841 TGAACACAGAGTAAAGAGAGCCTCATAGCCTGCGGGGGGCTGGCAAGCCACCCCAAGT 900
QY 901 CCTGTGCCCAAGAGGCGCTTCACTAGCCGCTCACTCTCTCCAGGAGCACTTTAGAAAGGT 960
Db 901 CCTGTGCCCAAGAGGCGCTTCACTAGCCGCTCACTCTCTCCAGGAGCACTTTAGAAAGGT 960
QY 961 TTTTAGCTAGTGTGTTTCTCTGCTTTTATAGACTCAGCCCGGCTGAGTGGCTAGAG 1020
Db 961 TTTTAGCTAGTGTGTTTCTCTGCTTTTATAGACTCAGCCCGGCTGAGTGGCTAGAG 1020
QY 1021 CCAGCAGGTGCGCATGTGCTACTGACAAAGTCTCAGCTTCCCGCGAGCCGGGCTCAGGC 1080
Db 1021 CCAGCAGGTGCGCATGTGCTACTGACAAAGTCTCAGCTTCCCGCGAGCCGGGCTCAGGC 1080
QY 1081 CGTGGAGCCGCTATATCTGCTCTCTGCTGCAAGACTCGTGGGGGCATCACAACCTGC 1140
Db 1081 CGTGGAGCCGCTATATCTGCTCTCTGCTGCAAGACTCGTGGGGGCATCACAACCTGC 1140
QY 1141 CCTGTGAGCGGAGCGGAGCCGAGCCTGTGTCTCTCACTCAGGTTGGCTTCCCTGTGC 1200
Db 1141 CCTGTGAGCGGAGCGGAGCCGAGCCTGTGTCTCTCACTCAGGTTGGCTTCCCTGTGC 1200
QY 1201 CCATGCTGTATGATCTGTGGGAGCACCAACCTGTGCGGAGTGGCTGCTCCG 1260
Db 1201 CCATGCTGTATGATCTGTGGGAGCACCAACCTGTGCGGAGTGGCTGCTCCG 1260
QY 1261 TGGTGTGAGGCGGGGCTGTGCTCATAGGCACTTCTGCTCCCAACCCCTGGCAGCA 1320
Db 1261 TGGTGTGAGGCGGGGCTGTGCTCATAGGCACTTCTGCTCCCAACCCCTGGCAGCA 1320
QY 1321 GGGAGAGGCTTGTGCTGACACACCCAGCTTATGTAATTTGAGTGTACTTAG 1380
Db 1321 GGGAGAGGCTTGTGCTGACACACCCAGCTTATGTAATTTGAGTGTACTTAG 1380
QY 1381 GAAGCCTTGGGAGAGGCGAGGCTGCCCATGCTCCCAAGCTGTGTGCGGAGTAT 1440
Db 1381 GAAGCCTTGGGAGAGGCGAGGCTGCCCATGCTCCCAAGCTGTGTGCGGAGTAT 1440
QY 1441 TATATAATCGTGGGAGAGATCCCGGCTGTGATGCTTTGGAGAGGAAATATGTTT 1500
Db 1441 TATATAATCGTGGGAGAGATCCCGGCTGTGATGCTTTGGAGAGGAAATATGTTT 1500
QY 1501 TCTCATTCGAAG 1512
Db 1501 TCTCATTCGAAG 1512

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RESULT 10
ACD29741
ID ACD29741 standard; cDNA; 1512 BP.
XX ACD29741;
XX AC ACD29741;
XX AC ACD29741;
XX DT 08-SEP-2003 (first entry)
XX DB Novel human secreted and transmembrane protein PRO615 cDNA.
XX XX Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW peripheral neuropathy; diabetic peripheral neuropathy;
KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW Refsum's disease; Abetalipoproteinemia; Tangier disease;

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KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy;
KW gene; ss.
OS Homo sapiens.
PN US2003050240-A1.
XX 13-MAR-2003.
PD 13-MAR-2003.
XX 16-OCT-2001; 2001US-00978403.
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
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PR 13-MAR-1998; 98US-0078004P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 30-APR-1998; 98US-0083742P.

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Db      361 TGCTATTGGTGAACCTGCTCTTCTCAAGCTCTCTGACCTTCTCTGGTTTGTGTTCT 420
Qy      421 GCTTCTCAACCAACAGTGGGAGTCAACCAACCGAAGAGAGTGTGGGGCCGACT 480
Db      421 GCTTCTCAACCAACAGTGGGAGTCAACCAACCGAAGAGAGTGTGGGGCCGACT 480
Qy      481 CTGTGAGGGAGAGCATACCTTCAGCTTCTTTTCATCTTCTCTGGGGGTGCTGGCT 540
Db      481 CTGTGAGGGAGAGCATACCTTCAGCTTCTTTTCATCTTCTCTGGGGGTGCTGGCT 540
Qy      541 CCTGGGCTTACAGCGCTTACAGGCTGGGCTGAGACGATTCATCCAGATTCAGTTGACC 600
Db      541 CCTGGGCTTACAGCGCTTACAGGCTGGGCTGAGACGATTCATCCAGATTCAGTTGACC 600
Qy      601 CCACTCCGGAGCCCAACACTGCTCCTACAGGCTGATCCAGATTCAGTTGAGCACTACC 660
Db      601 CCACTCCGGAGCCCAACACTGCTCCTACAGGCTGATCCAGATTCAGTTGAGCACTACC 660
Qy      661 AACAGCCACCTTACCCAGAGACGCGGAGACACCGAGGGCTACCAAGCCGCTGTGT 720
Db      661 AACAGCCACCTTACCCAGAGACGCGGAGACACCGAGGGCTACCAAGCCGCTGTGT 720
Qy      721 ACTGAGTGGGGTGAAGGTGGGAGAGGGGGACAGAGAGGGCCCTCCCTCTGGCCCTGACT 780
Db      721 ACTGAGTGGGGTGAAGGTGGGAGAGGGGGACAGAGAGGGCCCTCCCTCTGGCCCTGACT 780
Qy      781 TTCCCATCAGCTCTCTGGAACCTGCAAGCCCTCTCTTTCATCTGTTCACTCTGTGACAG 840
Db      781 TTCCCATCAGCTCTCTGGAACCTGCAAGCCCTCTCTTTCATCTGTTCACTCTGTGACAG 840
Qy      841 TGACACACACTTAAGAGAGCTCATAGCTGGGGGGCTGGGAGAGCCACACCCCAAGTG 900
Db      841 TGACACACACTTAAGAGAGCTCATAGCTGGGGGGCTGGGAGAGCCACACCCCAAGTG 900
Qy      901 CCGTGGCCAGAGGAGGCTTCACTAGTACGCGCTCACTCTCTCAAGGCACTTTAGAGAGGT 960
Db      901 CCGTGGCCAGAGGAGGCTTCACTAGTACGCGCTCACTCTCTCAAGGCACTTTAGAGAGGT 960
Qy      961 TTTTAGCTAGTGTTTTCTCTGCTTTTAATGACTCAAGCCGCTGCACTGTGAGTGAAG 1020
Db      961 TTTTAGCTAGTGTTTTCTCTGCTTTTAATGACTCAAGCCGCTGCACTGTGAGTGAAG 1020
Qy      1021 CCAAGCAGGTGCGCATGTGCTACTGACAAAGTGCCTGAGCTTCCCGCGGCGCGGATGAGG 1080
Db      1021 CCAAGCAGGTGCGCATGTGCTACTGACAAAGTGCCTGAGCTTCCCGCGGCGCGGATGAGG 1080
Qy      1081 CGTGGAGCGGCTAATTAATCTGCGTCTCTGCAAAAGACTGTGGGGCCATCACACTGC 1140
Db      1081 CGTGGAGCGGCTAATTAATCTGCGTCTCTGCAAAAGACTGTGGGGCCATCACACTGC 1140
Qy      1141 CCGTGGAGGGAGCGGAGCCAGGCTGTGTGCTCTCACTCAGGTTTGTCTCCCTGTGC 1200
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Qy      1201 CCACTGCTGATGATGTGGGGGACCAAGCTTTGTGCTCACTCAGGTTTGTCTCCCTGTGC 1260
Db      1201 CCACTGCTGATGATGTGGGGGACCAAGCTTTGTGCTCACTCAGGTTTGTCTCCCTGTGC 1260
Qy      1261 TGGGTGTAAGGGGCTGTGTGCTCACTGAGCACTTCTCTGCTCCACCCCTGGAGAGA 1320
Db      1261 TGGGTGTAAGGGGCTGTGTGCTCACTGAGCACTTCTCTGCTCCACCCCTGGAGAGA 1320
Qy      1321 GGGAGAGGCTTGTGCTGACAAACACCGAGCTTATGTAATATTCAGAGTTGTTACTTGA 1380
Db      1321 GGGAGAGGCTTGTGCTGACAAACACCGAGCTTATGTAATATTCAGAGTTGTTACTTGA 1380
Qy      1381 GAAAGCTGGGAGAGGAGGAGGAGTGGCCCAATGCTCTGTGTCGAGTGTAT 1440
Db      1381 GAAAGCTGGGAGAGGAGGAGGAGTGGCCCAATGCTCTGTGTCGAGTGTAT 1440
Qy      1441 TATAAATCGTGGGAGAGTCCCGGCTGGAGTGTGTTTGGAGACGGAATAATGTTT 1500
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Qy      1501 TCTCATTCGAAG 1512
Db      1501 TCTCATTCGAAG 1512

RESULT 11
ID ADAL2361 standard; cDNA: 1512 BP.
AC ADAL2361;
DT 06-NOV-2003 (first entry)
DE Human cDNA encoding secreted/transmembrane polypeptide PRO615.
XX ss; gene; inflammatory disease; organ failure; atherosclerosis;
XX cardiac injury; infertility; birth defect; premature aging; cancer;
XX diabetic complication; tissue typing; human.
OS Homo sapiens.
PN US2003055216-A1.
XX 20-MAR-2003.
XX
XX 17-OCT-2001; 2001US-00978824.
XX
XX 17-OCT-1997; 96US-0018049P.
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
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XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.

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[illegible]

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QY	1201	CCATGCTGTAATATCTGGGGGGCCACACCCTGGCCGCTGAGGCTGCTCCG	1260
Db	1201	CCAATGCTGTAATATCTGGGGGGCCACACCCTGGCCGCTGAGGCTGCTCCG	1260
QY	1261	TGCTGTGAAGGCGGGGCTGCTGCTCATATGACATCTCTTGGCTCCACCCCTGGAGCA	1320
Db	1261	TGGTGTAGAAGCGGGGCTGGTGTGTCAGGACATTCCTCTTGGCTCCACCCCTGGAGCA	1320
QY	1321	GGGAGAGGCTTTGGCTACACAACCCAGCTTTATGTAAATATCTGTCAGTGTACTTAG	1380
Db	1321	GGGAGAGGCTTTGGCTACACAACCCAGCTTTATGTAAATATCTGTCAGTGTACTTAG	1380
QY	1381	GAACCTGGGGAAGGCGAGGCTGCCATATGGCTCCGACATCTGTCGTGTCGCCAGTAT	1440
Db	1381	GAACCTGGGGAAGGCGAGGCTGCCATATGGCTCCGACATCTGTCGTGTCGCCAGTAT	1440
QY	1441	TATATAATTCGTGGGGAGATGCCCCGACCTGGATGCTGTTTGAGACGGAATAATGTT	1500
Db	1441	TATATAATTCGTGGGGAGATGCCCCGACCTGGATGCTGTTTGAGACGGAATAATGTT	1500
QY	1501	TCTCATTCGAAG	1512
Db	1501	TCTCATTCGAAG	1512

RESULT 12	
ACD29156	
1D	ACD29156 standard; cDNA; 1512 BP.
XX	
AC	ACD29156;
XX	
DT	27-AUG-2003 (first entry)
XX	
DE	Novel human secreted and transmembrane polypeptide cDNA #36.
XX	
KM	Human; secreted and transmembrane protein; PRO; viral infection;
KM	tumour growth; retinal disorder; injury; sight loss;
KM	retinitis pigmentosum; age-related macular degeneration;
KM	sport-related joint problem; articular cartilage defect; osteoarthritis;
KM	rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KM	kidney disorder; mesangial cell function; Berger disease; nephropathy;
KM	celiac disease; dermatitis; Crohn disease; neuropathy;
KM	diabetic insufficiency disorder; peripheral neuropathy;
KM	diabetic peripheral neuropathy; autonomic neuropathy;
KM	reduced motility of the gastrointestinal tract;
KM	atrophy of the urinary bladder; post polio syndrome; Krabbe's disease;
KM	Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KM	Refsum's disease; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2003049633-A1.
XX	
XX	13-MAR-2003.
PD	
PF	16-OCT-2001; 2001US-00978565.
XX	
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XX Human PRO polynucleotide sequence #36.  
DE  
XX  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW cell death; neuropathy; neuropathy related disease; Krabe's disease;  
KW Charcot-Marie-Tooth disorder; Refsum's disease; septic shock;  
KW chromosome mapping; gene mapping; genetic disorder; gene; ss.  
XX  
XX  
XX Homo sapiens.  
XX  
XX US2003083248-A1.  
XX  
XX  
XX 01-MAY-2003.  
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XX 16-OCT-2001; 2001US-00978757.  
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 PI Goodard A, Godowski PJ, Grimaldi JC, Gunney AU, Hillan KU,  
 PI Kijavini J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI: 2003-755118/771.  
 DR P-PSDB: ADB76384.  
 XX  
 PT New PRO polypeptides useful for treating peripheral neuropathy,  
 PT neuropathies associated with systemic disease such as post-polio syndrome  
 PT or AIDS-associated syndrome.  
 PT  
 PS Claim 2; Fig 60; 425bp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for  
 CC identifying agonists or antagonists. The bioactive molecule maybe a  
 CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides  
 CC are useful for treating neuropathy and neuropathy related diseases such  
 CC as Charcot-Marie-Tooth disorder, Reiter's disease, and Krabbe's disease.  
 CC The polynucleotide sequences encoding PRO polypeptides are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation

Query March 100.0%; Score 1512; DB 9; Length 1512;  
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Job time : 626 secs

GenCore version 5.1.6  
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Run on: April 8, 2004, 04:54:41 ; Search time 5848 Seconds

(without alignments)  
11206.338 Million cell updates/sec

Title: US-10-020-445A-161

Perfect score: 1512

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Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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DEFINITION Sequence 161 from Patent EP1241184.  
ACCESSION AX538190  
VERSION AX538190.1 GI:25270341  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.  
Human synapocogyrin-like protein and nucleic acids encoding the same  
Patent: EP 1241184-A 161 18-SEP-2002;  
JOURNAL

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Genentech, Inc. (US)
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Version	1			
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Source	FLI CDNA			
Organism	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Emmeryella; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins			
	A Bioinformatics Assessment			
	Genome Res. 13 (10), 2265-2270 (2003)			
JOURNAL	12975309			
PubMed	2 (bases 1 to 1512)			
REFERENCE	Clark,H.F.			
AUTHORS				

TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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gene  
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ORIGIN

Query Match 100.0%; Score 1512; DB 9; Length 1512;  
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ORIGIN
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LOCUS Homo sapiens synapcogyrin 2, mRNA (cDNA clone MGC:8571
DEFINITION

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Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,  
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 Generation and initial analysis of more than 15,000 full-length  
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 REFERENCE  
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 JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL  
 REMARK  
 COMMENT  
 Email: gga@bmc.tmc.edu  
 Tissue Procurement: Lou Strausberg  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
 Contact: amg@bcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,  
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 A.N., Gibbs, R.A.  
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**JOURNAL**

Submitted (26-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
(26-OCT-2002)

REFERENCE  
AUTHORS

3 (pages 1 to 158033)

## AUTHORS

Barrett, B., Hubbard, C., Lander, E., Allu, A., Allen, N., Anderson, S., Banna, N., Bastien, V., Bloom, T., Boguski, L., Bonkshalter, B., Camarero, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Delleraio, K., Dewar, K., Diaz, J. S., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galasari, J., Gardner, S., Gord, S., Graham, L., Grand, P., Hafez, N., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kages, A., Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, T., Matthews, C., McCarthy, M., Meldrum, J., Menzies, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., North, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retter, R., Riese, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, U., Tesfaye, S., Theodore, J., Toppan, K., Travers, M., Vassiliev, H., Veli, S., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (127-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jan 9, 2003 this sequence version replaced ar127476165.  
All repeats were identified using RepeatMasker:  
Shu, A. P. A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE  
JOURNAL

Direct Submission  
Sub: 14-1-1 / 127 WIT 2003) 171-10604 Trans: 14-1-10/MTT Center for Genome

COMMENT

On Jan 9, 2003 this sequence replaced gi:27476165  
All repeats were identified using RepeatMasker:

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WIBR

Center code: WIBH

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information -----

Center project name: L28450  
Center clone name: 100\_D\_13

Center clone name: 100\_D\_13

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone CTD-2022H16
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 80119)
Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barina,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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TITLE Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 80119)
Birren,B., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S.,
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Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (14-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 14, 2002 this sequence version replaced gi:18699917.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: 2022\_H\_16  
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VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

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REFERENCE
AUTHORS Birren, B., Nussbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 15, clone RP11-93209
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 188596)

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REFERENCE
AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Bouhagalter, B., Brown, A., Camarata, J., Campoliano, A., Chang, J.,
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
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Topham, K., Travers, M., Trava, N., Trigglio, J., Vassiliev, H.,
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TITLE Direct Submission
JOURNAL Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 188596)
Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhagalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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TITLE
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COMMENT

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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP13-598G7
Unpublished
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (26-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 163776)
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
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Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
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Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 24, 2002 this sequence version replaced gi:26190543.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/SW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 128453
Center clone name: 598_G_7

NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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* 61007 61106: gap of 100 bp
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 AUTHORS Fischer, C.L., Rosen, C.A., Soppet, D.R., Ruben, S.M., Kyaw, H., Li, Y., Zeng, Z., Lafleur, D.W., Moore, P.A., Shi, Y., Ols, H.S., Ebner, R. and Brewer, J.A.  
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REFERENCE 1 (bases 1 to 3052)
AUTHORS Ansoore,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1. D-85764 Neuberberg, GERMANY
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de,
Sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp666M214) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcententrum, Heuberweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
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Search completed: April 8, 2004, 08:53:45  
 Job time : 5860 secs



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/ APPLICANT: Stuart, Susan G.			
/ APPLICANT: Murry, Lynn E.			
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/ NUMBER OF SEQUENCES: 12			
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/ ADDRESSEE: Incyte Pharmaceuticals, Inc.			
/ STREET: 3174 Porter Drive			
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/ MEDIUM TYPE: Diskette			





RESULT 4  
US-09-713-550-135  
Sequence 135, Application US/09713550  
Patent No. 6617109  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C4  
CURRENT APPLICATION NUMBER: US/09/713.550  
CURRENT FILING DATE: 2000-11-14  
NUMBER OF SEQ ID NOS: 205  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 135  
LENGTH: 396  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-713-550-135

Query Match 25.6%; Score 386.4; DB 4; Length 396;  
Best Local Similarity 99.7%; Pred. No. 2.5e-81;  
Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 877 GCTGCGAGAGCCACACCCCAAGTGTGCTGCGCAGAGGGCTTCAGTACGCGCTCACTCC 936  
DB 9 GCTGCGAGAGCCACACCCCAAGTGTGCTGCGCAGAGGGCTTCAGTACGCGCTCACTCC 68  
QY 937 TCCAGGGCACTTTTGAAGAGGTTTAACTAGTGTTCCTCGCTTTAATGACTC 996  
DB 69 TCCAGGGCACTTTTGAAGAGGTTTAACTAGTGTTCCTCGCTTTAATGACTC 128  
QY 997 AGCCCGGCTGAGTGTGCTAGAGGCGACAGAGTGCCTACTGACCAAGTGCCTCA 1056  
DB 129 AGCCCGGCTGAGTGTGCTAGAGGCGACAGAGTGCCTACTGACCAAGTGCCTCA 188  
QY 1057 GCTTCCCCCGGGGCGGTCAAGCCGTGAGAGCCGCTTATATCTGCGTCTCTGCAAG 1116  
DB 189 GCTTCCCCCGGGGCGGTCAAGCCGTGAGAGCCGCTTATATCTGCGTCTCTGCAAG 248  
QY 1117 ACTCGTGGGGGCGCATCAACCTGCTGTGCGAGCGGACCGACCAAGGCTTGTGTCT 1176  
DB 249 ACTCGTGGGGGCGCATCAACCTGCTGTGCGAGCGGACCGACCAAGGCTTGTGTCT 308  
QY 1177 CACTCAGGTTTGCTTCCCTGTGCGCACTGTGTATGATCTGGGGGCGACCAAGCTGTGC 1236  
DB 309 CACTCAGGTTTGCTTCCCTGTGCGCACTGTGTATGATCTGGGGGCGACCAAGCTGTGC 368  
QY 1237 CGGTGGGCTCTGGGGGCTGCGCTCCCGTGT 1264  
DB 369 CGGTGGGCTCTGGGGGCTGCGCTCCCGTGT 396

RESULT 5  
US-08-700-637-11  
Sequence 11, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Murty, Susan G.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700.637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: LUNGN0T04  
CLONE: 809604  
US-08-700-637-11

Query Match 18.3%; Score 276.8; DB 2; Length 296;  
Best Local Similarity 97.3%; Pred. No. 9.3e-56;  
Matches 289; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 28 GCGGCGAGCGGCGGCGAGCGGCGACATGAGAGCGGGGCTACGCGCGGCGCAAGCGGCGG 87  
DB 1 GCGGCGAGCGGCGGCGGCGAGCGGCGACATGAGAGCGGGGCTACGCGCGGCGCAAGCGGCGG 60  
QY 88 GCTCTTGCACCTTGCAGGCGGCTTCTCTGACGACCGGAGGTGTGTGCGCGCGCGGTGTGT 147  
DB 61 GCTTCTTGCACCTTGCAGGCGGCTTCTCTGACGACCGGAGGTGTGTGCGCGCGCGGTGTGT 119  
QY 148 TGGTCTTGCCTTGCATGCTGCTTCTCTGACGACCTATGATGATGAGGGCTACAGCAATGCGCAAG 207  
DB 120 TGGTCTTGCCTTGCATGCTGCTTCTCTGACGACCTATGATGATGAGGGCTACAGCAATGCGCAAG 179  
QY 208 AGCTTAAGAGATGATAGTCTGCTGCTTCAACCGGACGAGATCCTGCGGCTTATGCAAGT 267  
DB 180 AGCTTAAGAGATGATAGTCTGCTGCTTCAACCGGACGAGATCCTGCGGCTTATGCAAGT 239  
QY 268 CCATCGGGGTGCTGGGCTTCTGCGGCTGCGGCTTCTTGTGTGTCAGCGGTAT 324  
DB 240 CCATCGGGGTGCTGGGCTTCTGCGGCTGCGGCTTCTTGTGTGTCAGCGGTAT 296

RESULT 6  
US-08-700-637-7  
Sequence 7, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Murty, Susan G.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: COLNCT01  
CLONE: 608493  
US-08-700-637-7

Query Match 17.3%; Score 261; DB 2; Length 265;  
Best Local Similarity 98.5%; Pred. No. 4.4e-52;  
Matches 261; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 57 AGCGGGGCTTACGCGCGCGCAAGCGGGGCGCTCTTCTGACCTGCGGCGCTTCTGACG 116  
Db 1 AGCGGGGCTTACGCGCGCGCAAGCGGGGCGCTCTTCTGACCTGCGGCGCTTCTGACG 60  
QY 117 CACCGCGAGGTGGTGGCGCGCGCGCTTCTGATGCTGCTTCTGCTTCTGCTTCTGCTG 176  
Db 61 CACCGCGAGGTGGTGGCGCGCGCGCTTCTGATGCTGCTTCTGCTTCTGCTTCTGCTG 120  
QY 177 ATCTATGTGAGGCTACAGCATGCCCAAGTCTAAGCATGATGCTGCTGCTTCTGCTG 236  
Db 121 ATCTATGTGAGGCTACAGCATGCCCAAGTCTAAGCATGATGCTGCTGCTTCTGCTG 180  
QY 237 CGCAAGAGAGATCCCTGCGCGCTATGCGAGTGCATGGGGTGGCTTCTGCGCTTCTG 296  
Db 181 CGCAAGAGAGATCCCTGCGCGCTATGCGAGTGCATGGGGTGGCTTCTGCGCTTCTG 240  
QY 297 GCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321  
Db 241 GCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265

RESULT 7  
US-08-700-637-6  
Sequence 6, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Murry, Susan G.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: MMLR2DT01  
CLONE: 476266  
US-08-700-637-6

Query Match 17.3%; Score 261; DB 2; Length 272;  
Best Local Similarity 96.0%; Pred. No. 4.5e-52;  
Matches 261; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 36 GCGCGGACGCGGACATGAGAGAGCGGGGCTTACGCGCGCGCAAGCGGGGCGGCTTCTG 95  
Db 1 GCGCGGACGCGGACATGAGAGAGCGGGGCTTACGCGCGCGCAAGCGGGGCGGCTTCTG 60  
QY 96 GACCTGCGGCGCTTCTCTGACGACCGCGAGGTGGTGGCGCGCGCTTCTGCTTCTGCTT 155  
Db 61 GACCTGCGGCGCTTCTCTGACGACCGCGAGGTGGTGGCGCGCGCTTCTGCTTCTGCTT 120  
QY 156 GCTTGTATCGTGTCTCTCTGATCTATGATGAGGGCTTACAGCATGCGGCGGCTTCTG 215  
Db 121 GCTTGTATCGTGTCTCTCTGATCTATGATGAGGGCTTACAGCATGCGGCGGCTTCTG 180  
QY 216 CAGATGATGCTGCTTCTCTGATCTATGATGAGGGCTTACAGCATGCGGCGGCTTCTG 275  
Db 181 CAGATGATGCTGCTTCTCTGATCTATGATGAGGGCTTACAGCATGCGGCGGCTTCTG 240  
QY 276 GTGCTGCGCTTCTCTGCGCTGCGCTTCTTCTT 307  
Db 241 GTGCTGCGCTTCTCTGCGCTGCGCTTCTTCTT 272

RESULT 8  
US-08-700-637-5  
Sequence 5, Application US/08700637  
Patent No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Murry, Susan G.  
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: TMR2DT01  
CLONE: 392250  
US-08-700-637-5

Query Match 15.2%; Score 229.4; DB 2; Length 232;  
Best Local Similarity 99.1%; Pred. No. 1e-44; 2; Indels 0; Gaps 0;  
Matches 230; Conservative 0; Mismatches 2;

Db 72 GCGGCCAAGGCGGCGCTCTTTCAGACCTGCGGCGCTTCTTCAAGCGAGCGGAGTGTG 131  
1 GCGGCCAAGGCGGCGCTCTTTCAGACCTGCGGCGCTTCTTCAAGCGAGCGGAGTGTG 60  
Qy 132 GCGGCCGCGCTGCTGCTGCTTCTTTCAGACCTGCGGCGCTTCTTCAAGCGAGCGGAGTGTG 191  
Db 61 GCGGCCGCGCTGCTGCTGCTTCTTTCAGACCTGCGGCGCTTCTTCAAGCGAGCGGAGTGTG 120  
Qy 192 TACAGCAATGCCGCGAGTCTAAGCAATGCTGCTGCTTCAAGCGAGCGGAGTGTG 251  
Db 121 TACAGCAATGCCGCGAGTCTAAGCAATGCTGCTGCTTCAAGCGAGCGGAGTGTG 180  
Qy 252 TGCGGCTATGCGAGTGCCTATGCGGCTGCTGCTTCTTCAAGCGAGCGGAGTGTG 303  
Db 181 TGCGGCTATGCGAGTGCCTATGCGGCTGCTGCTTCTTCAAGCGAGCGGAGTGTG 232

## RESULT 9

US-08-700-637-10  
Sequence 10, Application US/08700637

PATENT No. 5854413  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL SYNAPTOGRAIN HOMOLOG FROM COLON  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,637  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0065 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 230 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
LIBRARY: BRAUTUT02  
CLONE: 754306  
US-08-700-637-10

Query Match 14.5%; Score 219; DB 2; Length 230;  
Best Local Similarity 99.6%; Pred. No. 2.8e-42;  
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 54 GAGAGCGGGGCTACGAGCGCGGCGGAGCGGCGGCTCTTTCAGACCTGCGGCGCTTCTG 113  
Db 1 GAGAGCGGGGCTACGAGCGCGGCGGAGCGGCGGCTCTTTCAGACCTGCGGCGCTTCTG 60  
Qy 114 ACGAGCGCGGAGTGTGCGCGCGCGGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTCTC 173  
Db 61 ACGAGCGCGGAGTGTGCGCGCGGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTCTC 119  
Qy 174 TGCACTATGTGAGGGCTTACAGCAATGCCAGAGTCTAAGCAATGATGATGATGATGATG 233  
Db 120 TGCACTATGTGAGGGCTTACAGCAATGCCAGAGTCTAAGCAATGATGATGATGATGATG 179  
Qy 234 AACCGCAAGAGGATGCTGCGGCTATGCGAGTGCATGCGGAGTGTGCTG 284  
Db 180 AACCGCAAGAGGATGCTGCGGCTATGCGAGTGCATGCGGAGTGTGCTG 230

## RESULT 10

US-09-620-312D-317  
Sequence 317, Application US/09620312D

PATENT No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehman, Tom  
APPLICANT: Xue, Aidiang J.  
APPLICANT: Yang, Jionglong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yunding  
APPLICANT: Wang, Dairui  
APPLICANT: Wang, Zhilue  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION DATE: 2000-04-25  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pc\_Fl\_genes Version 1.0  
SEQ ID NO 317  
LENGTH: 1639  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (93) .. (668)  
US-09-620-312D-317

Query Match 14.5%; Score 218.8; DB 4; Length 1639;  
Best Local Similarity 64.1%; Pred. No. 5.3e-42;  
Matches 364; Conservative 0; Mismatches 197; Indels 7; Gaps 2;

Qy 4 ACGCGTGGCGGACGCGT-GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 62

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Db      45  ACGGCTCCGCCACGCGCTCCGGGGGACCGCGGGTCCAGCCACGATGGAAGGGGGT 104
Qy      63  GCCTACGCGCGCGCAAGCGCGGGGCGTCTCTGACCTGCGGGGCTTCTGACGACCGG 122
Db      105  GCGTACGAGACGGGCAAGCGGGGGCGCTTCCAGCCCTACACCCCTGGTCCGGACCGG 164
Qy      123  CAGGTGGTGGCGCGCGCGTGTGCTTGTGCTTGGCCCTGATCGTGTTCCTGATCTAT 182
Db      165  CACACCACTCTGCGCGTGTGTCTTGGCTGTCTCCATAGTGTGTGTGGCTCCATCTG 224
Qy      183  GGTAGGAGCTACAGCAATGCCCAGAGTCTAAGAGATGACTGCGTGTCAACCGCAAC 242
Db      225  AACGAGGGCTACCTCAACAGCGCTCCGAGGGGGAGAGTGTGCAATCTACACCGCAAC 284
Qy      243  GAGATACCTTGGCGCTTATGCGAGTGCATGGGGGTGTGCGCTTCTGCGCTTGGCGCTT 302
Db      285  CCCAACGCTGCACTATGGCGTGTGGCGGTGTGTGCTGCGCTTCTGCACTGCTGCTG 344
Qy      303  TTCTTGTGTGCGAGCGGTATTTCCCGCAGATCAGCAACGCACTGACGCGCAAGTACTG 362
Db      345  TACCTGGCGCTGACCGTGTACTTCCCGCAGATCAGACGCGTCAAGACGCGCAAGAAC 404
Qy      363  GTCAATGTGACCTGCTCTTCTGACCTCTGGAACCTTCTGTGTGTGTGTGTGTGTG 422
Db      405  GTCTGTGCCACACATCGGTGTGTCTGCGCTTCTGCGCTTCTGTGTGTGTGTGTGTG 464
Qy      423  TTCCTACCAACAGTGGGAGTCAACCAACCGCAAGGAC-----GTGCTGTGTGGGGGCG 476
Db      465  TACCTGACCAACAGTGGGAGTCTCAAGCCCAAGCAACCACTGAACGAGGAGAG 524
Qy      477  GACTGTGTGAGGAGGAGGCAATACCTTCACTTCTTCACTTCTGCGGTGTGTGCTG 536
Db      525  GACGACACCGCGGGCGCGCATGCGCTTCTCTTTTCTCCATCTTCACTGAGACCTGAC 584
Qy      537  GCCGCCCTGGCGCTACGACGCGCTCAAGG 564
Db      585  GCAGCCTGGCGGTGGGAGATTCAAGG 612

RESULT 11
US-08-700-637-12
; Sequence 12, Application US/08700637
; Patent No 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara U.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 12:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: LUNGASt01
; CLONE: 868416
US-08-700-637-12

Query Match      14.1%; Score 213; DB 2; Length 339;
Best Local Similarity 95.4%; Pred. No. 7,7e-41;
Matches 228; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

Qy      47  CGACATGAGAGCGGGGCTTACGCGCGGCCCAAGCGGGGCGCTTCTGACCTTGGCGG 106
Db      1  CGACATGAGAGCGGGGCTTACGCGCGGCCCAAGCGGGGCGCTTCTGACCTTGGCGG 60
Qy      107  CTTCCTGACGAGCGCGAGGTGTGGGGCGCGCGGTGTGCTTGTGCTTGGCTTGTGATGT 166
Db      61  NTTCCTGACGAGCGCGAGGTGTGGGGCGCGCGGTGTGCTTGTGCTTGTGATGT 120
Qy      167  GTTCTCTGATCTATGTGTGAGGGCTTACGCAATGCCACGAGTCTTAAGCAGATGTACTG 226
Db      121  GTTCTCTGATCTATGTGTGAGGGCTTACGCAATGCCACGAGTCTTAAGCAGATGTACTG 180
Qy      227  CGTGTTCACCGGCAACGAGATGCTGCGCTATGAGATGSCATCGGGGTGTGCGCT 285
Db      181  CGTGTTCACCGGCAACGAGATGCTGCGCTATGAGATGSCATCGGGGTGTGCGCT 237

RESULT 12
US-08-700-637-9
; Sequence 9, Application US/08700637
; Patent No 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara U.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAT03

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Qy 319 CGATATTCCTCCGATGAGCAAGGCGACCTGACCGCAGTACTGTCATTTGTCACCTCG 378
Db 332 TGTACTTCCCGCATGACGAGCTCTCAAGACCGCAAGAAAGCCGTCCTCTCCGACATCG 391
Qy 379 TCTTTCAGCTCTCTGACCTTCTGATTTGTTGTTTCTGCTTCTTCCACCAACAGT 438
Db 392 GTGCTCGGCTTCTGAGCTTCTCTGTTCTGTTGAGATTCTGCTACCTGCGCAACAGT 451
Qy 439 GGGAGATCAACCAACCGAAGAC-----GTGCTGTTGGGGGCGGACTCTGTAGAGGACG 492
Db 452 GCGAGCTCTCAACCGCAAGACCAACCACTGAACGAAGAGAGAGAGCGAGCCCGGCGG 511
Qy 493 CCATACCTTCACTTCTTTCATCTTCTCTGAGGTTGCTGAGCTCCCTGAGCTTACC 552
Db 512 CCATCGGCTTCTCTTCTTCTTCTTCTTCACTTCACTGAGACCTGACCGAGCCCTGAGTGG 571
Qy 553 AGGCTTCAAG 564
Db 572 GGAGATTCAAG 583

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## RESULT 15

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US-09-620-312D-318
Sequence 318, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Duntui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 318
LENGTH: 842
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(609)
US-09-620-312D-318

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Query Match 11.5%; Score 174; DB 4; Length 842;

Best Local Similarity 64.7%; Pred. No. 1,3e-31;

Matches 277; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

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Qy 143 GTGCTTGTCTTCCCTTGTATGTTCTCTCTGATCTAAGGAGGCTACAGCAATGC 202
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Qy 203 CCAGAGTCTAAGAGATGTACTGCTGTTCAACCGCAAGAGATGCTGCGCTATGG 262

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Db 246 CGTGGCCGTGGGCGTGTCTGAGCTTCTTCTTCTTCTGCTGCTGCTGAGAGTGTATA 305
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Qy 383 CTGAGCTCTCTGAGCTTCTGAGTGTGTTGTTGTTTCTGCTTCTTCAACCAACAGTGGC 442
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Qy 443 AGTCACCAACCGAAGAGC-----GTGCTGTTGGGGGCGGACTGTGAGAGGAGCAT 496
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Qy 497 CACCTTCACTTCTTTCATCTTCTCTGAGGTTGCTGAGCTTCTCTGAGCTTCAACAG 556
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Search completed: April 8, 2004, 08:56:17  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2004, 11:56:24 ; Search time 42 Seconds  
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1400.711 Million cell updates/sec

Title: US-10-020-445A-162

Perfect score: 1191

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1071772 segs, 26263353 residues

Total number of hits satisfying chosen parameters: 1071772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1191	100.0	224	9 US-09-978-295A-162	Sequence 162, App
2	1191	100.0	224	9 US-09-978-697-162	Sequence 162, App
3	1191	100.0	224	9 US-09-978-192A-162	Sequence 162, App
4	1191	100.0	224	9 US-09-999-832A-162	Sequence 162, App
5	1191	100.0	224	10 US-09-978-189-162	Sequence 162, App
6	1191	100.0	224	10 US-09-978-608A-162	Sequence 162, App
7	1191	100.0	224	10 US-09-978-585A-162	Sequence 162, App
8	1191	100.0	224	10 US-09-978-191A-162	Sequence 162, App
9	1191	100.0	224	10 US-09-978-403A-162	Sequence 162, App
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13	1191	100.0	224	10 US-09-978-824-162	Sequence 162, App
14	1191	100.0	224	10 US-09-918-585A-162	Sequence 162, App
15	1191	100.0	224	10 US-09-978-423A-162	Sequence 162, App

16	1191	100.0	224	10 US-09-978-193A-162	Sequence 162, App
17	1191	100.0	224	10 US-09-999-830A-162	Sequence 162, App
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32	1191	100.0	224	12 US-09-999-831A-162	Sequence 162, App
33	1191	100.0	224	14 US-10-017-081A-162	Sequence 162, App
34	1191	100.0	224	14 US-10-167-749-162	Sequence 162, App
35	1191	100.0	224	14 US-10-013-921A-162	Sequence 162, App
36	1191	100.0	224	14 US-10-013-929A-162	Sequence 162, App
37	1191	100.0	224	14 US-10-016-177A-162	Sequence 162, App
38	1191	100.0	224	14 US-10-166-709A-162	Sequence 162, App
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40	1191	100.0	224	14 US-10-143-030A-162	Sequence 162, App
41	1191	100.0	224	14 US-10-002-967A-162	Sequence 162, App
42	1191	100.0	224	14 US-10-017-083A-162	Sequence 162, App
43	1191	100.0	224	14 US-10-145-128A-162	Sequence 162, App
44	1191	100.0	224	14 US-10-017-191A-162	Sequence 162, App
45	1191	100.0	224	14 US-10-143-028A-162	Sequence 162, App

## ALIGNMENTS

RESULT 1  
US-09-978-295A-162  
Sequence 162, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Klavirin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978, 295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585





PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
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 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 9; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 8,9e-123;  
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 VGPFELNQMAVINPKVILVAGDSVRAALTFSPFSIFSWGLASLAVQRYKAGVDPEIQ 180  
 DB 121 VGPFELNQMAVINPKVILVAGDSVRAALTFSPFSIFSWGLASLAVQRYKAGVDPEIQ 180  
 QY 181 YVDTPTDNTYASYPRGASVUNYQCPPTQMAETTBEGYQPPVY 224  
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RESULT 2  
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 Sequence 162, Application US/09978697  
 Patent No. US20020169284A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyere, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gunney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
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 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2630P1C27  
 CURRENT APPLICATION NUMBER: US/09/978,697  
 CURRENT FILING DATE: 2001-10-16  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1191; DB 5; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 8,9e-123; Indels 0; Gaps 0;  
 Matches 224; Conservative 0; Mismatches 0;

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 DB 1 MESSAGYAKKAGSGDIBRFLTPQVAVAVCLVFAIIVFSGIYGEYSNABSKOMTCV 60  
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 DB 61 FNRNEDACRYGSAIGVLAFLASAPFLVVDAYEPQISNATDRKYLIVIGDILTSALMTFLWF 120  
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RESULT 3  
 US-09-978-192A-162  
 Sequence 162, Application US/09978192A  
 Patent No. US2002017753A1  
 GENERAL INFORMATION:  
 APPLICANT: Aeshkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Geritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavitt, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.